
 WPSRCH

 (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 15:40:20 2000; Maspar time 25.93 Seconds
 Tabular output not generated. 936.964 Million cell updates/sec

Title: >US-09-235-416-1
 Description: (1-784) from US09235416A.pep
 Perfect score: 5472
 Sequence: 1 MSGGNGKVVVPNPARE.....ELRQQQAEALAKAQEP 784
 Scoring table: PAM 150
 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swiseprot

Statistics: Mean 54.902; Variance 108.067; scale 0.508

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	2217	40.9	1	KFIB_MOUSE KINESIN-LIKE PROTEIN K	0.00e+00
2	2175	40.1	1690	1 KFA1_HUMAN KINESIN-LIKE PROTEIN K	0.00e+00
3	2176	40.1	1695	1 KFA1_HUMAN KINESIN-LIKE PROTEIN K	0.00e+00
4	2051	37.8	1103	1 KFC1_HUMAN KINESIN-LIKE PROTEIN K	0.00e+00
5	1975	36.4	1584	1 U104_CAEEL KINESIN-LIKE PROTEIN U	0.00e+00
6	1008	18.6	699	1 K122_STRPU KINESIN-II 65 KDA SUBU	3.40e-173
7	962	17.7	701	1 KFA3_MOUSE KINESIN-LIKE PROTEIN K	1.37e-163
8	926	17.7	702	1 KFA3_MOUSE KINESIN-LIKE PROTEIN K	9.35e-163
9	926	17.7	702	1 KFA3_MOUSE KINESIN-LIKE PROTEIN K	1.03e-161
10	953	17.6	985	1 K1ML_FICHI KINESIN-LIKE PROTEIN K	1.78e-161
11	945	17.4	747	1 KFB3_HUMAN KINESIN-LIKE PROTEIN K	4.78e-160
12	942	17.4	747	1 KFB3_HUMAN KINESIN-LIKE PROTEIN K	2.02e-159
13	897	16.5	786	1 FL40_CHLRE KINESIN-LIKE PROTEIN F	4.60e-150
14	870	16.0	784	1 K1P4_MOUSE KINESIN-LIKE PROTEIN K	1.71e-139
15	846	15.6	1231	1 K1P4_MOUSE KINESIN-LIKE PROTEIN K	1.84e-144
16	839	15.5	672	1 OSM3_CAEEL KINESIN-LIKE PROTEIN O	4.80e-138
17	842	15.5	1232	1 K1P4_HUMAN KINESIN-LIKE PROTEIN K	1.15e-138
18	815	15.0	948	1 K1NH_NEUCR KINESIN HEAVY CHAIN	4.35e-133
19	799	14.7	2663	1 K1NE_HUMAN CENTROMERIC PROTEIN E	8.66e-130
20	762	14.1	805	1 YGNE_YEAST PUTATIVE KINESIN-LIKE	3.54e-122
21	766	14.1	935	1 K1NL_SYNRA KINESIN HEAVY CHAIN (S	5.34e-123
22	754	13.9	893	1 YB3D_SCHPO PUTATIVE KINESIN-LIKE	1.55e-120
23	747	13.8	160	1 KFC1_MOUSE KINESIN-LIKE PROTEIN K	4.24e-119

24	741	13.7	967	1 K1NL_LOLPE KINESIN HEAVY CHAIN	7.19e-118
25	731	13.5	1031	1 K1NL_STRPU KINESIN HEAVY CHAIN	8.04e-116
26	727	13.4	793	1 KFC3C_MOUSE KINESIN-LIKE PROTEIN K	5.29e-115
27	724	13.4	796	1 KFC3C_MOUSE KINESIN-LIKE PROTEIN K	2.18e-114
28	725	13.4	815	1 K1NL_CAEEL KINESIN HEAVY CHAIN	1.36e-114
29	715	13.2	796	1 KFC3C_RAT KINESIN-LIKE PROTEIN K	1.51e-112
30	707	13.0	975	1 K1NL_CHROME KINESIN HEAVY CHAIN	6.48e-111
31	704	13.0	1032	1 K1NL_HUMAN NEURONAL KINESIN HEAVY	2.66e-110
32	687	12.9	1027	1 K1NL_MOUSE NEURONAL KINESIN HEAVY	2.12e-109
33	668	12.9	1027	1 K1NL_MOUSE NEURONAL KINESIN HEAVY	2.12e-109
34	665	12.3	963	1 K1NL_MOUSE KINESIN HEAVY CHAIN (U	2.32e-102
35	656	12.1	1057	1 K1NL_MOUSE KINESIN-RELATED MOTOR	3.97e-100
36	656	12.1	1060	1 EG51_XENLA KINESIN-LIKE PROTEIN K	1.56e-100
37	648	12.0	776	1 K1P1_CHLRE KINESIN-LIKE PROTEIN K	6.53e-99
38	633	12.0	1066	1 K1L61_CHROME BIPOLAR KINESIN KRP-13	6.33e-100
39	652	12.0	1067	1 EG52_XENLA KINESIN-LIKE PROTEIN E	1.01e-99
40	649	12.0	1184	1 B1MC_DMENI KINESIN-LIKE PROTEIN B	4.09e-99
41	645	11.9	643	1 CPK2_XENLA CARBOXY-TERMINAL KINES	2.65e-98
42	627	11.6	754	1 KATC_ARATH KINESIN-LIKE PROTEIN C	1.16e-94
43	623	11.5	745	1 KATB_ARATH KINESIN-LIKE PROTEIN B	7.46e-94
44	616	11.4	770	1 K1PA_DMENI KINESIN-LIKE PROTEIN K	1.93e-92
45	602	11.1	832	1 K1P1_SCHPO KINESIN-LIKE PROTEIN I	1.28e-89

ALIGNMENTS

RESULT 1
 ID KFIB_MOUSE STANDARD; PRT; 1150 AA.
 AC Q60575;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE KINESIN-LIKE PROTEIN KFIB.
 GN KFIB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=BRAIN;
 RA MEDLINE; 45094296
 RA Nishikawa K, Saito-Yoshitake R., Okada Y., Noda Y., Takemura R.,
 Yamaoka H, Nishikawa K, Nishikawa R, Nishikawa K, Nishikawa K,
 *KFIB: a novel microtubule plus end-directed monomeric motor protein
 for transport of mitochondria.*;
 RL Cell 79:1209-1220(1994).
 CC -/- FUNCTION: MOTOR FOR ANTEROGRADE TRANSPORT OF MITOCHONDRIA. HAS A
 CC -/- MICROTUBULE PLUS END-DIRECTED MOTILITY.
 CC -/- SUBUNIT: MONOMER.
 CC -/- SUBCELLULAR LOCATION: PREDOMINANTLY FOUND ON THE VESICLE- AND
 CC TUBULE-LIKE STRUCTURES WITHIN THE CYTOPLASM.
 CC -/- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIN
 CC TISSUE (MAINLY IN THE CEREBELLUM AND CEREBRUM) WITHIN A SINGLE
 CC TYPE OF NEURONAL CELL.
 CC -/- SIMILARITY: CONTAINS 1 FHA DOMAIN.
 CC -/- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-104
 CC SUBFAMILY.

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EMBL; D17577; BAA04503.1;
 HSSP; P56536; 2KIN.
 MGD; MGI:108426; KIFIB.
 PFAM; PF00498; FHA; 1.
 PFAM; PF00225; Kinesin; 1.
 PRINTS; PR00380; KINESINHEAVY.
 PROSITE; PS00411; KINESIN_MOTOR_DOMAIN; 1.

DR PROSITE; P500067; KINESIN MOTOR_DOMAIN2; 1.
 DR PROSITE; P500006; FHA_DOMAIN; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 1 355 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 FT DOMAIN 359 380 COILED COIL (POTENTIAL).
 FT DOMAIN 424 456 COILED COIL (POTENTIAL).
 FT DOMAIN 510 566 FHA.
 FT DOMAIN 622 663 COILED COIL (POTENTIAL).
 FT DOMAIN 814 858 COILED COIL (POTENTIAL).
 FT NP_BIND 97 104 ATP (POTENTIAL).
 SQ SEQUENCE 1150 AA; 130278 MW; 5AA426DAFEBD252F CRC64;

Query Match 40.9%; Score 2217; DB 1; Length 1150;
 Best Local Similarity 55.3%; Pred. No. 0.00e+00;
 Matches 340; Conservative 132; Mismatches 114; Indels 29; Gaps 20;

Db 1 MSGAS-VKVVYVRPNPNSRETSKESKCIQMGNSTIINP-----R--NP-K---EAPK 48
 QY 1 MSGGGIKVYVRPNPAREIDRGACIVRMENQITLTPPGAEEKARKSKTMDGPK 60
 Db 49 SFSDYSYNSHTSPEDPCFASQRVYNDIGKEMLLHAFEGYWCIFAYGQTGACKSYTAM 108
 QY 61 AFAPDSYNSFDR-NAPNARYQEDLFDLPGLLONAFKYNCTFAYGQTGSKSYSM 119
 Db 109 GKQESQAVIIPOLCELFKIND-NCEEMSYSEVSYMEIYCERVDLLPNKGNLR 167
 QY 120 GYKGE-HGYI-PRICODMFRINELOKDKNLCTVEYSLEYINERVDLLNPSTKGNLK 177
 Db 168 VREHPLGPGYVEDLKLAVTSYTDIADLDAGNARKARTVAATNNNETSSSRSHAVFTLTQ 227
 QY 178 VREHPTGPGYVEDLKLAVTSYTDIADLDAGNARKARTVAATNNNETSSSRSHAVFTLTQ 237
 Db 228 KQDPETNLSTKYSKISLVLDAGSERADSTGAKTRKEGANINKSLITLTKVISALAE 287
 QY 238 KWHDETKMDTKVAKISLVLDAGSERATSTGATGARLKEGAEINRSLSLTGRVIAALAD 297
 Db 288 VSK-KKKTKDFIPYRDSVLTNLLRENGGNSRTAMVAALSPADINDTSLTRYADRAK 346
 QY 298 MSGGKQKQLVYRDSVLTNLLKSLGSGNSMTAMIAISPADINFEETLSLTRYADSAK 357
 Db 347 QIKGNVINEPDAKLVRELKVEVTRKDLRAQGLDI-IDTSGSLTSS--PSSCSLNS 404
 QY 358 RIKRHAVNEDPNARIRELKEELAKSLGSGGGGGAGSGGSGGVEEYPPDTPLEK 417
 Db 405 QVGLTSYISIGRINSTPGGEAIELEKSEKIAELNETWEKLRTEAIMEERALLA 464
 QY 418 QI-SIQOPNTVYKMSKAB-IVQLNGSKERYLDNLTWEKLAETIEHKREAALE 474
 Db 465 EAGVALREDQGTGVESKTKTHLYNLNEDPLMSCLLYIKGTITGVGQDAERODIV 524
 QY 475 ELGISI-E-KGVGVPKSKEMPHLNLSDPLLAELVYINPGQTRGVNQVQDQNR 532
 Db 525 LSGAHKEHCLERSRNGEVIVTLPECSERSEYTNKRVAPHVOLSGNRLKKNH 584
 QY 533 LNSGLKLEHCTF-E--NVDNV-VTIYPNKAAYNGVYIDKPTRLASGRYIILGDHF 587
 Db 585 VRENHPQEARERE 599
 QY 588 IFRNHPQEARERQ 602

RESULT 2
 ID KFLA HUMAN STANDARD; PRT; 1690 AA.
 AC 012756;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE KINESIN-LIKE PROTEIN KIFIA (AXONAL TRANSPORTER OF SYNAPTIC VESICLES).
 GN KIFIA OR ATSV.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]

SEQUENCE FROM N.A.
 TISSUE-BRAIN:
 RX Furlong R.A., Zhou C.Y., Ferguson-Smith M.A., Affara N.A.;
 RA "Characterization of a kinesin-related gene ATSV, within the tuberous
 RL sclerosis locus (TSC1) candidate region on chromosome 9Q34."; Genomics 33:421-429(1996).
 CC -1- FUNCTION: MOTOR FOR ANTEROGRADE AXONAL TRANSPORT OF SYNAPTIC
 CC VESICLE PRECURSORS (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-104
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 FHA DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
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 CC
 CC EMBL; X90840; CAA62346.1;
 DR HSP; P17119; 3KAR.
 DR MTM; 60125;
 DR PFAM; PF00498; FHA; 1.
 DR PFAM; PF00169; PH; 1.
 DR PFAM; PF00225; kinesin; 1.
 DR PROSITE; P00380; KINESINHEAVY.
 DR PROSITE; P500411; KINESIN MOTOR_DOMAIN1; 1.
 DR PROSITE; P500067; KINESIN MOTOR_DOMAIN2; 1.
 DR PROSITE; P50003; PH_DOMAIN; 1.
 DR PROSITE; P500006; FHA_DOMAIN; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 1 361 MECHANOCHEMICAL (MOTOR).
 FT DOMAIN 366 383 COILED COIL (POTENTIAL).
 FT DOMAIN 429 462 COILED COIL (POTENTIAL).
 FT DOMAIN 516 572 FHA.
 FT DOMAIN 622 681 COILED COIL (POTENTIAL).
 FT DOMAIN 801 822 COILED COIL (POTENTIAL).
 FT DOMAIN 1575 1673 PH.
 FT NP_BIND 97 104 ATP (POTENTIAL).
 SQ SEQUENCE 1690 AA; 191083 MW; D8DDEC784624FB4D CRC64;

Query Match 40.1%; Score 2175; DB 1; Length 1690;
 Best Local Similarity 54.1%; Pred. No. 0.00e+00;
 Matches 335; Conservative 131; Mismatches 122; Indels 31; Gaps 19;

Db 1 MAGAS-VKVVYVRPNPNSRETSKESKCIQMGNSTIINP-----R--NP-K---EAPK 48
 QY 1 MSGGGIKVYVRPNPAREIDRGACIVRMENQITLTPPGAEEKARKSKTMDGPK 60
 Db 49 SFSDYSYNSHTSPEDINASQVYRQIEGMLOHAFEGYWCIFAYGQTGACKSYTAM 108
 QY 61 AFAPDSYNSFDR-NAPNARYQEDLFDLPGLLONAFKYNCTFAYGQTGSKSYSM 119
 Db 109 GKQESQAVIIPOLCELFKIND-NCEEMSYSEVSYMEIYCERVDLLPNKGNLR 167
 QY 120 GYKGE-HGYI-PRICODMFRINELOKDKNLCTVEYSLEYINERVDLLNPSTKGNLK 177
 Db 168 VREHPLGPGYVEDLKLAVTSYTDIADLDAGNARKARTVAATNNNETSSSRSHAVFTLTQ 227
 QY 178 VREHPTGPGYVEDLKLAVTSYTDIADLDAGNARKARTVAATNNNETSSSRSHAVFTLTQ 237
 Db 228 KQDPETNLSTKYSKISLVLDAGSERADSTGAKTRKEGANINKSLITLTKVISALAE 287
 QY 238 KWHDETKMDTKVAKISLVLDAGSERATSTGATGARLKEGAEINRSLSLTGRVIAALAD 297
 Db 288 MSGGKQKQLVYRDSVLTNLLRENGGNSRTAMVAALSPADINDTSLTRYADRAK 346
 QY 298 MSGGKQKQLVYRDSVLTNLLKSLGSGNSMTAMIAISPADINFEETLSLTRYADSAK 352

[illegible]

15-DEC-1998 (rel. 37, Last sequence update)
15-DEC-1998 (rel. 37, Last annotation update)
KINESIN-LIKE PROTEIN KIFC.
GN
KIFC.
OS
Homo sapiens (Human).
OC
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
CC
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC
[1]
CC
SEQUENCE FROM N.A.
CC
TISSUE=HIPPOCAMPUS;
CC
MEDLINE; 98352063.
CC
Dorner C., Glossek T., Mueller S., Moeller N.P.H., Ullrich A.,
CC
Lammers R.;
CC
"Characterization of KIFC, a new kinesin-like protein involved in
CC
vesicle transport from the Golgi apparatus to the endoplasmic
CC
reticulum.";
CC
J. Biol. Chem. 273:20267-20275 (1998).
CC
-1- FUNCTION: MOTOR REQUIRED FOR THE RETROGRADE TRANSPORT OF GOLGI
CC
VESICLES TO THE ENDOPLASMIC RETICULUM. HAS A MICROTUBULE PLUS END-
CC
SUBUNIT MONOMER. (POTENTIAL).
CC
-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED, WITH MOST
CC
ABUNDANT EXPRESSION IN HEART AND SKELETAL MUSCLE.
CC
-1- PWM: PHOSPHORYLATED ON TYROSINE.
CC
-1- SIMILARITY: CONTAINS 1 FHA DOMAIN.
CC
-1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-104
CC
SUBFAMILY.
CC

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CC
EMBL; 091329; AAC52117.1;
CC
MIM; 603060;
CC
DR
MIM; 603060; FHA; 1.
CC
DR
PFAM; PF00439; Kinesin; 1
CC
DR
PROSITE; PS00430; KINESIN_HEAVY
CC
DR
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN; 1
CC
DR
Motor domain. Microtubules, ATP-binding; Coiled coil;
CC
Phosphorylation.
CC
KW
Phosphorylation.
CC
FT
DOMAIN 1 355 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
CC
FT
DOMAIN 359 388 COILED COIL (POTENTIAL).
CC
FT
DOMAIN 438 479 COILED COIL (POTENTIAL).
CC
FT
DOMAIN 523 575 FHA.
CC
FT
DOMAIN 633 674 COILED COIL (POTENTIAL).
CC
FT
DOMAIN 828 872 COILED COIL (POTENTIAL).
CC
FT
NP_BIND 97 104 COILED COIL (POTENTIAL).
CC
FT
SEQUENCE 1103 AA; 1233071 MW; F148C398D428C10 CRC64;
CC
SQ

	228	RCHQDLTGDSKPKYSKLIVLDAGSERDSSGARGNRUKRGANIKSUTLTKVKVISALAD	281
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	238	KHWDDETMDTKEVAKISLVLDAGSERSTGTATGARUKRGEINLSLTARGVIALAD	297
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	288	MOS--KKKSDPTPEYRSVLTVTLKENLGNSPNTAIAI SPADI NYETILSTRVDRHK	346
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	298	KSSGQKKQKVLPVPYRSVLTVLLKSGSGNSMTAITAI SPADI NYETILSTRVASAK	357
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	347	QLRCNATIINEDPNARILRISEEVARELLAMAGGISASALEGLKTGGSVRGALPAVS	406
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	358	RKNHIAVNVEDPNARMIRLEELAOLSKL--OS-SGGG-GG--GAGSGG-SPVEE-SY	409
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	407	PPAPVSPSSPTTHNGELPEPSNPNTSOIGPEAFMERLOTEKIIAEINLWEEELAKTE	466
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	410	PPD--TPLE--KQTVSIQOP--DA-TVKKMKSAIEVQLNGSEKLRYDLNQWEEELAKTE	463
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	467	ALRMERALLIAMGVAVRDGSGTVGFSPKTPHLVNLINEDPLIMSECILYHKDKGVTRVG	526
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	464	EIHKERFAALELAGIST-EKG-FVGYFHSKEMPHVNLSDPLLACLVLYNIKPGQVRG	521
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	527	QV--DM--DIKLQTQFRHQHCIFRSIPDPQGEVVVTLPCEGAETTYNGKLTPELVLK	582
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	522	NYNDQTOAIRUNGSKLKECHTFENV--D-NW-TIVPEKAAYVNVGRIDKPTRLR	576
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	583	SGNIYVGNKHVFRRNHPQARJERE	608
Db		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	577	SGYRLILGDHFIRFNHPPEARMRQ	602
Qy		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
	5		
RESULT			
ID	U104_CAEEL	STANDARD;	PRT; 1584 AA.
AC	P23678;		
DC	01-NOV-1991 (Rel. 20, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	KINESIN-LIKE PROTEIN UNC-104.		
DN	UNC-104.		
GC	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;		
ON	Rhabdilitidae; Peloderinae; Caenorhabditis.		
RN	[]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 91097805.		
RA	Otsuka A.J., Jayaprakash A., Garcia-Anoveros J., Tang L.Z., Fisk G.,		
RA	Thorne T., Franco R., Born T.		
RT	"The C. elegans unc-104 gene encodes a putative kinesin heavy		
RT	chain-like protein."		
RT	Neuron 6:113-122(1991).		
CC	-!- FUNCTION: INVOLVED IN MICROTUBULE-ASSOCIATED TRANSPORT.		
CC	-!- SIMILARITY: CONTAINS 1 FH DOMAIN.		
CC	-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. UNC-104		
CC	CLASSIFICATION:		

```

FT DOMAIN 425 445 COILED COIL (POTENTIAL).
FT DOMAIN 598 652 COILED COIL (POTENTIAL).
FT DOMAIN 777 797 COILED COIL (POTENTIAL).
FT DOMAIN 183 335 MICROTUBULE-BINDING.
FT DOMAIN 1460 1558 PH.
FT DOMAIN 957 1052 ARG/LYS-RICH (BASIC).
FT DOMAIN 1203 1584 ARG/LYS-RICH (BASIC).
FT NP_BIND 93 100 ARG (BY SIMILARITY).
FT VARIANT 598 598 ATP (BY SIMILARITY).
FT VARIANT 930 930 I -> T.
FT SEQUENCE 1384 AA: 179736 MW: 53946233FD029B43 CRC64;
Query Match 36.48; Score 1975; DB 1; Length 1584;
Best Local Similarity 52.68; Pred. No. 0.00e+00;
Matches 318; Conservative 123; Mismatches 126; Indels 38; Gaps 20;

Db 2 SSVKAVVRFPNOREISNTSKVLOVNGNTTIN--G--HSLNKE-N-F-----SFNF 49
Qy 5 GNTKVVVRFPNAREIDMGKAFKRVMEGNTTLTPPPGAERKAKSGKTKIDGKFAF 64
Db 50 DHSYASFPNDPHITQKQVVEELGEMLEHAFEGYNCVFAYQGTGSKSYTMKGAND 109
Qy 65 DRYSDYFNKNAPYARQEDFODLGVPLDADNAPYKNCVFAYQGTGSKSYTMKG--YG 122
Db 110 PDMGITPRLCNLPKADN-NNUKQVQSVESYWEIYCYERKVDLLNPNSGKNLRYREN 168
Qy 123 KEH-GYPLQCDNFRINELQRNUTCTVYSLEITNERNVADLNPSTAGNLAYREN 181
Db 169 PLLGQVDDLTAKVCSYHDCINLADGKAKARTVAATNNKSTSSSRSHAVFTVLTQK 228
Qy 182 PSTGQVYEDLAKLVSPFOBIENLADGKAKARTVAATNNKSTSSSRSHAVFTVLTQ 241
Db 229 ADSNLTDEKHSKISLVLDAGSRANSTGAEGRLKEGANINKSLTTLGLVSKLAESTK 288
Qy 242 EETKMDTEKAVKISLVLDAGSRATSTGATGARKEGAEINRSLTGLRVIALADMSG 301
Db 289 KKKSGKGVIPYRDSVLTWLRNLGGNSKTMALALSPADINFDETSLTRYADAKQIV 348
Qy 302 KKKNO-LVPRYRDSVLTWLRNLGGNSKTMALALSPADINFDETSLTRYADAKRIK 360
Db 349 QAVVNDENPAKILRELNEZYKLRHLKDG-----IDVTD--VDET--PGK--HKK-G 396
Qy 361 NHAVNEEDNPMIRRELKEAQLRSKLOSSGGGGGAGGGGPGVEEIPPTPLEKQIV 420
Db 397 P-KLP-AHYH---EOL-EKLOSEKLMAGTYWROKLIHWERIKOREEELRDNGLAC 449
Qy 421 SIQPDATVKKMSAEIVDQALQSEKLYDNLQWTEKLEKATTEELIKEREALAEIGIS- 479
Db 450 AEDGTLTGVSFKPLHVLNMDPLMSCLITLYLEKGVTSVGRPEAHPDILLGSAI 509
Qy 480 IERGF-VGPYSKEMPHLVNLSDDPLASCLVLYNPKPGQTRVGNVQDQAEIRLNGSI 538
Db 510 LEIKCFEINEDGNTYITMKPNASCVINQGVYTPVTLHTSGSVILGEHVFYNDPOEAR 569
Qy 539 LKECHTFENDVNTYIVPNEKAAYVNGVRIDKPTLRSCYRITLADGFIFRNFHPEAR 598
Db 570 OSRHN 574
Qy 599 AEQGE 603

RESULT 6
ID K122_STRPU STANDARD; PRT: 699 AA.
AC P46872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE KINESIN-II 85 KDA SUBUNIT (KRP-85/95 85 KDA SUBUNIT).
GN KRP85.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidae;
OC Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.

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RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE-EGG;
RX MEDLINE: 94050179.
RA Cole D.G., Chinn S.W., Wedaman K.P., Hall K., Vuong T.,
RA Scholey J.M.;
RT *Novel heterotrimeric kinesin-related protein purified from sea
RT urchin eggs.*;
RL Nature 366:268-270(1993).
CC -1- SUBUNIT: TRIMER OF A 115 KDA SUBUNIT AND TWO KINESIN-LIKE SUBUNITS
CC OF 95 AND 85 KDA.
CC -1- FTH: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC -1- SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L16993; AAA16098.1; -.
DR BSSP: P17119; JKAR.
DR PRAM: P00225; Kinesin; 1.
DR PRITIS: P00380; KINESINHEAVY.
DR PROSITE: PS00467; KINESIN_MOTOR_DOMAIN; 1.
DR PROSITE: PS00467; KINESIN_MOTOR_DOMAIN; 1.
KW MOTOR protein; Microtubules; ATP-binding; Coiled coil.
FT DOMAIN 1 340 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
FT DOMAIN 341 619 COILED COIL (BY SIMILARITY).
FT DOMAIN 620 699 GLOBULAR (BY SIMILARITY).
FT NP_BIND 97 104 ATP (POTENTIAL).
FT SEQUENCE 699 AA: 78697 MW: 763866111CB08190 CRC64;
Query Match 18.6%; Score 1008; DB 1; Length 699;
Best Local Similarity 45.0%; Pred. No. 3.40e-173;
Matches 182; Conservative 86; Mismatches 111; Indels 25; Gaps 15;

Db 6 SGDNVVRVVRCPINLSKTSQGFKSVYKNDENRG--TVQV-TNPAP-SG----EPPKS 57
Qy 2 SGGGKIVVVRPVRPAGRIKACIVRMENQNTILPPPGAEKARKSGRTIMDGKFA 61
Db 58 FTFD-T--VF--ARG-AKQTDYQTPARTVDALTEGYNCTIFAYQGTGKTFYNEG- 109
Qy 62 PAFDSYSDFNKNAPYARQEDFODLGVPLDADNAPYKNCVFAYQGTGSKSYTMKG 121
Db 110 VRSOPELHGIIPNSFAHIFSHIAKQENPFLVRVSYLEYNEVKOLLGQDQHRLEVK 169
Qy 122 GREHGVIPRICQDNPRRI-NELQDK-NLCTVEVSYLEYNEVRVOLLNPKTGKLAVR 179
Db 170 ERPOGVGVYKDLASFAFVYNADMDRIITLGNKNRSVGATNNNESSSHAFITL-ERS 228
Qy 180 EHPSTGTFVEDLAKLVRFQFETENLMDENGNKARTVAATNNKSTSSSRSHAVFTV 239
Db 229 DMGLDEQIRVGVKLIHWDLAGSERQTKTCATGQRKLEATKINLSLTGLNVISSLPV-- 286
Qy 240 HDEETKNQTEKAVKISLVLDAGSERATSTGATGARKEGAEINRSLTGLRVIALADMS 299
Db 287 -OK--STH-IPTRNSKTLRLLOSGLGNATVNCANIGPARYWDETISTLRVANKNI 342
Qy 300 SGKQKNKQVPRYDSVLTWLRNLGGNSKTMALALSPADINFDETSLTRYADAKRI 359
Db 343 KKKAKINDEPKALLREFOKELKEELKQJSESGSGLLDDDESGS 386
Qy 360 KHAVVNEEDNPMIRRELKEAQLRSKLOSSGGGGGAGGGSGG 403

RESULT 7
ID K33A_MOUSE STANDARD; PRT: 701 AA.
AC P28741;
DT 01-DEC-1992 (Rel. 24, Created)

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DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE KINESIN-LIKE PROTEIN KIF3A (MICROTUBULE PLUS END-DIRECTED KINESIN MOTOR 3A).
 GN KIF3A OR KIF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE; 93077686.
 RA Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hirokawa N.; *Kinesin family in murine central nervous system.*;
 RL J. Cell Biol. 119:1287-1296(1992).
 CC -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING ACTIVITY IN VITRO.
 CC -!- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIN TISSUE (MAINLY IN THE CEREBELLAR GRANULAR LAYER) WITHIN A SINGLE TYPE OF NEURONAL CELL.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
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 CC EMBL; D12645; BAA02166.1; .
 DR PIR; B44259; B44259.
 DR HSP; P56536; KIF3A.
 DR MG1; 107589; KIF3A.
 DR PFAM; P00225; kinesin; 1.
 DR PRO380; KINESINHEAVY
 DR PROSITE; P50041; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; P50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW Motor Protein; Microtubules; ATP-binding; Coiled coil; Neurons
 FT DOMAIN 351 530 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 FT DOMAIN 587 766 COILED COIL (BY SIMILARITY).
 FT DOMAIN 100 107 GLOBULAR (BY SIMILARITY).
 FT NP_BIND 100 107 ATP (BY SIMILARITY).
 FT DOMAIN 442 445 POLY-GLU.
 FT DOMAIN 509 512 POLY-GLU.
 SQ SEQUENCE 701 AA; 80167 MW; 2405872DF2D85A29 CRC64;
 Query Match 17.78; Score 962; DB 1; Length 701;
 Best Local Similarity 41.48; Pred. No. 137e-163;
 Matches 196; Conservative 104; Mismatches 137; Indels 36; Gaps 28;
 Db 14 NVKVVVRCPLNRE--K-SWCY-K-QAV-SV-DEMRCIT-TVHKTDSSN-EPKPTFTD 64
 Qy 6 NIKVVVVPFNAREIDRGAKCIYVMEGNTILTPPGAEEKARKSKTINDGPKAFAD 65
 Db 65 -T--VF--GPE-SKOLDVY-NLTARPTIDSVLEGYNGTIFAYGOTGKTFTMEGVRAV 116
 Qy 66 RSVKSFDPKNAPYARQEDLDQGLV-PLLDNAFYGNCFAYGOTGSGKYSNMGY-G- 122
 Db 117 PLGLRGVFNPSFAHGFHGHAKAEDTRFL--VRVSYLEYINEVRDLGKQDTORLVEKVR 174
 Qy 123 KE-HGVIPRICQDMFRRINELQKDNLTCTVSEVSYLEYINERVRDLINFTKGNLKVREH 181
 Db 175 PDGVGVYIKDLSAVYNNADMDIRMTLGHKNSVGNATNNHSSRSHALFTITTECKSG 234
 Qy 182 PSTGPTVEDLAKLVRSFOEINLMDGCKARTVAATNNKETSRSRSHAVFTLTQKWH 241
 Db 235 VDCGNMHV-RMGKLVHLDAGSRQAKTGQORLKAATKINLSLSTLGNVTSALVD--G 290
 Qy 242 EETKNDTEKVAKISLVLDAGSRATSTGATGARLKEGAEINSLSTLGRVLAALADMSG 301

Db 291 K--STH-VPYRNSKILTRLLQDSLGNSKTMCMANIGPADYNYDETISTLRVANRKN 347
 Qy 302 KQKKNQLPVYRDSVLTMLKDSLGNSMTAAIAISPADINFEETSLTRVADSARKIKN 361
 Db 348 KAKINDEPKAALLRQFKEIEELKKLEE--GVEVSDISQSEDDDE--EGELGDEKRR 405
 Qy 362 HAVVNEDNARMITRELKELAQLRSLQSGGGGGGGGGGSGPVEESYPPDTPEKQIVS 421
 Db 406 KRRDQAGKKVSPDKWE-M-QA-KIDEE--RKALETKLQWEERENKRAELE 454
 Qy 422 IQQPDATVKKMSKAEIVQLNQSEKLYRDLNQTWEEKLAKTEIHKREAALE 474
 RESULT 8
 ID KIF3A HUMAN STANDARD; PRT; 702 AA.
 AC Q9V496;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE KINESIN-LIKE PROTEIN KIF3A (MICROTUBULE PLUS END-DIRECTED KINESIN MOTOR 3A).
 DE KIF3A.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=RETINA;
 RA Wang S.Y., Bost-Usinger L., Hoang E., Frazer K.A., Reichelt S., Burnside B.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING ACTIVITY IN VITRO.
 CC -!- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
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 CC EMBL; AF041853; AAC72234.1;
 DR PROSITE; P50041; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; P50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW Motor Protein; Microtubules; ATP-binding; Coiled coil; Neurons
 FT DOMAIN 351 587 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 FT DOMAIN 588 702 GLOBULAR COIL (BY SIMILARITY).
 FT NP_BIND 100 107 ATP (BY SIMILARITY).
 FT DOMAIN 443 446 POLY-GLU.
 SQ SEQUENCE 702 AA; 80337 MW; 24507D1EC6D540DB CRC64;
 Query Match 17.78; Score 958; DB 1; Length 702;
 Best Local Similarity 40.89; Pred. No. 9.35e-163;
 Matches 193; Conservative 107; Mismatches 138; Indels 35; Gaps 27;
 Db 14 NVKVVVRCPLNRE--K-SWCY-K-QAV-SV-DEMRCIT-TVHKTDSSN-EPKPTFTD 64
 Qy 6 NIKVVVVPFNAREIDRGAKCIYVMEGNTILTPPGAEEKARKSKTINDGPKAFAD 65
 Db 65 -T--VF--GPE-SKOLDVY-NLTARPTIDSVLEGYNGTIFAYGOTGKTFTMEGVRAI 116
 Qy 66 RSVKSFDPKNAPYARQEDLDQGLV-PLLDNAFYGNCFAYGOTGSGKYSNMGY-GK 123
 Db 117 PLGLRGVFNPSFAHGFHGHAKAEDTRFL--VRVSYLEYINEVRDLGKQDTORLVEKVR 174
 Qy 124 -E-HGVIPRICQDMFRRINELQKDNLTCTVSEVSYLEYINERVRDLINFTKGNLKVREH 181

Db 175 PDGVVTKDLSAYVNNADMDRIWTLGHKNSVGTAVNNHSSRSRSHAFITITBCSEKG 234
 Qy 182 PSTGYVEDLAKLVLSVQSFQVNAEIDRGAKCIVPMEGNQTILTPPGCAEKARKSKTINDQPKAF 62
 Db 235 IDGNMHW-RNGKRLHVLDAISROKATGQORLKEATKINISLSTLGNISALVD---G 290
 Qy 242 EETKMDYEVAKISVLDVLAGSERATSGTARLKEGATNRSLSLSTLGRVIAALADMSG 301
 Db 291 K-STH-VYVRNSKRLRLQDLSGNSKTMPCANIGPADYWDDETISTLRYANRAKNIKN 347
 Qy 302 KOKKQLVPTDYSVLLWLLSGNSMTAMIAISPADINFEETLSTLRADSAKRKN 361
 Db 348 KASINEDPDKALLPOKEITPELKKLEP-GEIISGDSISGEEDDEEVEGEDEKKR 406
 Qy 362 HAYVEDPNARMIRBELKEALQRLSKLOSSGGGGAGGSGGCPVEESYPTPLEKQTVS 421
 Db 407 KRIIOIGKKVSPDKME-W-QA-KIDEP-RKALETKLDMEEERKARLE 455
 Qy 422 IQQPDPTVKNKSAKEIVQLNQSEKLYRLDQNLQWEEKLAKTEIHKEREALIE 474
 RESULT 9
 ID K12LSTRPU STANDARD; PRT; 742 AA.
 AC P46871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-DEC-1996 (Rel. 37, Last annotation update)
 DE KINESIN-II 95 KDN SUBUNIT (KRP-B5/95 95 KDN SUBUNIT).
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidae;
 OC Strongylocentrotidae;
 OC Strongylocentrotus.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=EGG;
 RX MEDLINE; 94050179.
 RA Cole D.G., Chinn S.W., Wedaman K.P., Hall K., Vuong T.,
 RA Scholey J.M.;
 RT "Novel heterotrimeric kinesin-related protein purified from sea
 urchin eggs.";
 RL Nature 366:268-270(1993).
 CC -1- SUBUNIT: TRIMER OF A 115 KDA SUBUNIT AND TWO KINESIN-LIKE SUBUNITS
 CC OF 95 AND 85 KDA.
 CC -1- OF 95 AND 85 KDA SUBUNIT IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
 CC II SUPERFAMILY.
 CC -----
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 CC or send an email to licensese@isb-sib.ch).
 CC -----
 CC EMBL; U00996; AAA87393.1; .
 CC HSSP; P56536; 2KIN.
 DR PRINTS; PR00380; kinesin; 1.
 DR PROSITE; PS00367; KINESIN-MOTOR DOMAIN1; 1.
 DR PROSITE; PS00411; KINESIN-MOTOR DOMAIN2; 1.
 KW MOTOR protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 1 337 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 FT DOMAIN 338 613 COILED COIL (BY SIMILARITY).
 FT DOMAIN 614 742 GLOBULAR (BY SIMILARITY).
 FT NP_BIND 95 102 ATP (POTENTIAL).
 FT REPEAT 742 AA; 84202 W; 47C40A367BAA77B5 CRC64;
 SQ SEQUENCE 17.7%; Score 962; DB 1; Length 742;
 Query Match Best Local Similarity 44.5%; Pred. No. 1.37e-163;
 Matches 177; Conservative 86; Mismatches 105; Indels 30; Gaps 18;

Db 5 SAETVAVVYVRCNMSKELSGHRIKRVEMDNKRG-LVEVTNP--KGP-PGEP--N--KSF 56
 Qy 3 GGGIXVYVYVRFVNAEIDRGAKCIVPMEGNQTILTPPGCAEKARKSKTINDQPKAF 62
 Db 57 TFDVVDNN-SKQIDLV---DETFRSL-V---ESVLOGFNGCTIFAYGTGKTFTMGV 108
 Qy 63 AFDIST-NSFDKNAPNAQEDLPDGLVPLDNFAKGYNNCTFAYGTGSGKSYSMGY 121
 Db 109 RSNPELRGVSPNSFEHIFTARTNQOFL---VRASYLEYTQEEIRDLADOKRDL 165
 Qy 122 --K-E'G-PRICQDMFRINELQDKNKTCTVEVSYLEYTINERVRLDLPSTGRNKL 178
 Db 166 KERDPQGVYKDLDSFYVSKVEIHEVMTVGNNRKSVGSTMNHSRSHAFITITICS 225
 Qy 179 REHSTGTPYEDLAKLVLSVQSFQVNAEIDRGAKCIVPMEGNQTILTPPGCAEK 238
 Db 226 ELVGDEGNIH-RVGLKLVLDLAGSERATSGTARLKEGATNRSLSLSTLGRVIA 283
 Qy 239 WIDEETKMDYEVAKISVLDVLAGSERATSGTARLKEGATNRSLSLSTLGRVIA 298
 Db 284 --GK--SSH-IPYRDSKRLRLQDLSGNSKTMPCANIGPADYWDDETISTLRYAN 338
 Qy 299 SSGKQKQLVPTDYSVLLWLLSGNSMTAMIAISPADINFEETLSTLRADSAKR 358
 Db 339 INKPKINQDLDALLREFQEEISRLKQALDKKGPSDG 376
 Qy 359 IKNHVVNEDPNARMIRBELKEALQRLSKLOSSGGGG 396
 RESULT 10
 ID K1NLSEICH STANDARD; PRT; 955 AA.
 AC P4685;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE KINESIN-LIKE PROTEIN K39 (FRAGMENT).
 GN KIN.
 OS Leishmania chagasi.
 OC Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HMOB/BR/92 / ISOLATE BA-2;
 RX MEDLINE; 9313867.
 RA Burns J.M. Jr., Shreffler W.G., Benson D.R., Chalh H.W., Badaro R.,
 RA Need S.G.;
 RT "Leishmania chagasi: characterization of a kinesin-related antigen of
 Leishmania visceral leishmaniasis.";
 RT American visceral leishmaniasis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
 CC -1- DEVELOPMENTAL STAGE: PREDOMINANT IN AMASTIGOTES.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; L07879; AAA29254.1; .
 CC HSSP; P70119; KIN39.
 DR PRINTS; PR00325; kinesin; 1.
 DR PROSITE; PS00411; KINESIN-MOTOR DOMAIN1; 1.
 DR PROSITE; PS00067; KINESIN-MOTOR DOMAIN2; 1.
 KW MOTOR protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 1 399 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 FT DOMAIN 426 >955 COILED COIL (POTENTIAL).
 FT NP_BIND 122 129 ATP (POTENTIAL).
 FT DOMAIN 704 >955 7 X 39 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 704 742 1.
 FT REPEAT 743 781 2.

FT REPEAT 782 820 3.
 FT REPEAT 821 859 4.
 FT REPEAT 860 898 5.
 FT REPEAT 899 937 6.
 FT REPEAT 938 >955 7 (PARTIAL).
 FT NON_TER 955 955
 SQ SEQUENCE 955 AA; 106168 MW; 8CA76815B84C6E9 CRC64;

Query Match 17.6%; Score 953; DB 1; Length 955;
 Best Local Similarity 43.5%; Pred. No. 1.03e-161;
 Matches 177; Conservative 90; Mismatches 111; Indels 29; Gaps 18;

Db 13 VKVVRVPRNERENNAPECTKVTYAAQAQAAVTVYKVLGSSNNSGAESMGTAARVAQD 72
 Qy 7 IKVVVRVPRNAREID-R-GAKCIVR-MEQNTI-LTPPPGAEEKARKSGK-TIMCPKA 61

Db 73 FQFDHVFVSTPDACGATPAQADVFRTGTVYQVHAFDGFNSCLFAYGTGSGKTYTM 132
 Qy 62 FAFDRSYNFK-N-A-PNY-AQEDLQDGLGVPLLDNAEKGYNCIFAYGTGSGKSYM 118

Db 133 MGADYSALSSEGGNGVTRICLETFAKASVEAQAQGSWIVELGVYVEYVNRVSDLGKRR 192
 Qy 119 MG-----Y-GKEGVIPRICQDMFRNELQDKNITCTVEVSYLEYNERVOLL-NP- 170

Db 193 KGVKGGEVYVDVREHPSRGVLEG-ORLVFVGLSDVYVRLIEIGNGVHRTAKMNR 251
 Qy 171 -STYK---NL-KVREHPSGTVYEDAKLV-VRSFOETENIMDEGNKARTVAATNNET 223

Db 252 SSRSHATMLLREERTMTKSGMTFRTAGKSSRMNLVDLAGSERVAQSQVQEQFKAT 311
 Qy 224 SSRSHAVFTLTLQKW---HDEETKMDTEKAKISLVLDLAGSERATSTGATGARKLKA 279

Db 312 HINLSLTGLRVIVLADMATKGAQYVAPFRDLSKLTFLKDSLGSGSKTPIATVSP 371
 Qy 280 EIRNSLTGLRVITLADAMS-GROKNQQLVYRDYSVLTWLLKDSLGSGSKTPIATVSP 338

Db 372 SALNVEETSLTYASRARDIVNVAQVNDPRARRIRELEQMEDMR 418
 Qy 339 ADINFEETSLTYADSARKINHAHVNDPNARMIRKELKELAQLR 385

RESULT 11
 TO KFB3_HUMAN STANDARD; PRT; 747 AA.
 AC Q5066; 1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 36, Last annotation update)
 DE KINESIN-LIKE PROTEIN KIF3B (MICROTUBULE PLUS END-DIRECTED KINESIN MOTOR 3B) (K19A0359) (H0048).
 DE MOTOR 3B)
 GN KIF3B
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP TISSUE-BRAIN
 RC SEQUENCE FROM N.A.
 RX MEDLINE: 97349984
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.",
 RL DNA Res. 4:141-150(1997)
 CC -1- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING ACTIVITY IN VITRO (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
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 CC -----
 CC EMBL: AB002357; BAA20815.1;
 CC HSP: P56536; 2KIN.
 CC MIM: 603754;
 CC PFAM: PF00225; kinesin; 1;
 CC PRINTS: P00380; KINESIN MOTOR DOMAIN; 1;
 CC PROSITE: PS00411; KINESIN MOTOR DOMAIN; 1;
 CC Motor protein; Microtubules; ATP-binding; Coiled coil; Neurone.
 KW DOMAIN 345 345
 FT DOMAIN 346 579
 FT DOMAIN 580 747
 FT NP_BIND 96 103
 FT DOMAIN 386 393
 FT POLY-GLY.
 FT DOMAIN 394 406
 FT POLY-SER.
 FT DOMAIN 723 730
 SQ SEQUENCE 747 AA; 85125 MW; 97FA4573AFA87023 CRC64;

Query Match 17.4%; Score 945; DB 1; Length 747;
 Best Local Similarity 47.0%; Pred. No. 4.78e-160;
 Matches 164; Conservative 72; Mismatches 99; Indels 14; Gaps 9;

Db 37 KLGQSVKNPKGTAAHMPKFTTFDAVDWNAQPELYDETERPLVDSVLQGFNGTIFAYG 96
 Qy 50 KSGKTIIMDGPKAFADRS-YWSEFDKNAPYARQEDLQDGLGVPLLDNAEKGYNCIFAYG 108

Db 97 QTGTGKTYMBEGIRGDPKRGVYINPSFDHFTHSRSQNOYL---VRASYLEYQYEIR 153
 Qy 109 QTSGSGSKSMGYG-QK-E-HGVIPRICQDMFRINELQDKNLCTCTVEVSYLEYNERVR 165

Db 154 DLLSKDQTKLEIKERPDGTGVYVQKLSFVTSKYEIEHVHVGNGNRSGVATNNHSS 213
 Qy 166 DLLNSTPGKINLVREHPSGTGYVEDLAKLVRSFOETENIMDEGNKARTVAATNNETS 225

Db 214 RSHAIVFTI-ECSEVGLDGENHIVRGLNLDVLAGSERQAKTGAGSERKATKATKLNLSL 272
 Qy 226 RSHAIVFTITLQKHDEETKMDTEKAKISLVLDLAGSERATSTGATCARKEGAEINRSL 285

Db 273 SALGNVISALVD---GK--STH-IPYRDKSLTRLQDSLGGNAKTVNVAANGSPASYNVEE 326
 Qy 286 STIGRVIAALADSSGKQKNQVLYRDSVLTWLLKDSLGSGNSMTAMIAISPADINFE 345

Db 327 TLTLLRYANRAKINKNRPVNDPKDALLREFQBEIARLKAOLKRSIG 375
 Qy 346 TLTSLRYADSARKINHAHVNDPNARMIRKELKELAQLRKLSQSSGG 394

RESULT 12
 TO KFB3_MOUSE STANDARD; PRT; 747 AA.
 AC Q61771; 1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE KINESIN-LIKE PROTEIN KIF3B (MICROTUBULE PLUS END-DIRECTED KINESIN MOTOR 3B).
 DE MOTOR 3B).
 GN KIF3B
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-ICR; TISSUE-BRAIN;
 RC MEDLINE: 96032268
 RA Yamazaki H., Nakata T., Okada Y., Hirokawa N., "KIF3A/B: a heterodimeric kinesin superfamily protein that works as a microtubule plus end-directed motor for membrane organelle transport.",
 RL J. Cell Biol. 130:1387-1399(1995).
 CC -1- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING

CC ACTIVITY IN VITRO.
 CC -I- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC -I- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II. SUBFAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D26077; BAA05070.1; --
 CC HSSP: P56536; 2KIN
 CC MCD: MG1:107688; KIF3B.
 CC PFAM: PF00225; kinesin.1.
 CC PRINTS: PR00380; KINESINHEAVY.
 CC PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1;
 CC PROSITE: PS00067; KINESIN_MOTOR_DOMAIN2; 1;
 CC Motor protein; Microtubules; ATP-binding; Coiled coil; Neurons.
 CC KW DOMAIN 1 345 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 CC FT DOMAIN 346 579 COILED COIL (BY SIMILARITY).
 CC FT DOMAIN 580 747 GLOBULAR.
 CC FT NP-BIND 96 103 ATP (POTENTIAL).
 CC FT DOMAIN 386 393 POLY-GLY.
 CC FT DOMAIN 394 405 POLY-GLU.
 CC FT DOMAIN 723 730 POLY-SER.
 CC SEQUENCE 747 AA; 85288 MW; FA369A4190ECB847 CRC64;
 CC -----
 CC Query Match 17 48; Score 942; DB 1; Length 747;
 CC Best Local Similarity 46.7%; Pred No. 2,02e-159;
 CC Matches 163; Conservative 73; Mismatches 99; Indels 14; Gaps 9;
 CC -----
 CC Db 37 KLGQVSVKPNKGTSHMEKTFEFDVYDNNAKOFLYDETRPLVDVLOGENGTIFAVG 96
 CC Qy 50 KSGKITNDKPAFAFDRS-VNFSFKNAPNVARQEDFDGLGVPLLDNAFKNCFIATG 108
 CC -----
 CC Db 97 QTGTGKTYTMEGVGRDPEKRGVPIGNSFDHIFTHIRSGNOQVL---VRASYLEYIYEETR 153
 CC Qy 109 OTSGCKSYSMGWY-GK-E-HGVIPRICQDFRINELQKDKNLCTCTVEYLEYINERV 165
 CC -----
 CC Db 154 DLLSKDQTKRLEKRPDPTGVYVYKDLSSFVTKSVKEIHEVMVNGNSYGAETMNEHSS 213
 CC Qy 166 DLLNFTSGNKLKRVSTPVEDIAKLIVRSFOETENLMDENSKARTVAATNMNTSS 225
 CC Db 214 RSHAFVITL-ESEVGLDGEHIVKTNKLVLDAGSRQAKTGAQGERKAEKYNLSL 272
 CC Qy 226 RSHAFVITLTKQKHDEETMOTKVKALISVLDAGSRATSTGATGRULGASINSL 285
 CC -----
 CC Db 273 SALGNVTSALVD---GK--STH-TPYRDSKITLLOQSLGGNKAATVYANVGSPATNVEE 326
 CC Qy 286 STLGVIAALADSSCKKNQNLVPRVSVLTWLLKSLGGSNTMTAIAISPANFEE 345
 CC -----
 CC Db 327 TLTLRTYANRKNKPKRVNEDPKALREFOREIARLKAQLEKRSIG 375
 CC Qy 346 TLTLRYADSAKRKNHAYVNEPDMRTRELKESLAQLRSKLQSSGG 394
 CC -----
 CC RESULT 13
 CC ID KL68-DROME STANDARD; PRT; 784 AA.
 CC AC P46867; 1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DR 15-JUL-1998 (Rel. 36, Last annotation update)
 CC DE KINESIN-LIKE PROTEIN KL68B.
 CC OS KL68B OR KLPS.
 CC GN Drosophila melanogaster (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC OC Ephydroidea; Drosophilidae; Drosophila.
 CC RP SEQUENCE FROM N.A.

RY MEDLINE: 95050960
 RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;
 RT "Characterization of the Klp68D kinesin-like protein in Drosophila:
 RT possible roles in axonal transport.";
 RL J. Cell Biol. 127:1041-1048(1994).
 RN [2]
 RP SEQUENCE OF 220-342 FROM N.A.
 RX MEDLINE: 92020874.
 RA Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;
 RT "Identification and partial characterization of six members of the
 RT kinesin superfamily in Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
 RN -I- UNIDIRECTIONAL PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR
 CC ANTERIOR-POSTERIOR TRANSPORT COULD CONVEY CYTOSOLIC MOVING CARGOES IN
 CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR
 CC OTHER PLUS-END DIRECTED MOTORS.
 CC -I- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS
 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
 CC EMBRYOGENESIS.
 CC -I- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U15974; AAA69929.1; --
 CC HSSP: P56536; AAA28658.1; --
 CC PFAM: PF00225; kinesin.1.
 CC PRINTS: PR00380; KINESINHEAVY.
 CC PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1;
 CC PROSITE: PS00067; KINESIN_MOTOR_DOMAIN2; 1;
 CC Motor protein; Microtubules; ATP-binding; Coiled coil.
 CC KW DOMAIN 16 275 MECHANOCHEMICAL (MOTOR).
 CC FT DOMAIN 351 385 COILED COIL (POTENTIAL).
 CC FT DOMAIN 426 582 COILED COIL (POTENTIAL).
 CC FT NP-BIND 106 113 ATP (POTENTIAL).
 CC FT CONFLICT 220 221 SS -> TC (IN REF. 2).
 CC FT CONFLICT 338 342 GSRK -> BRGV (IN REF. 2).
 CC SEQUENCE 784 AA; 88193 MW; 94BB9ABD072DFC0 CRC64;
 CC -----
 CC Query Match 16.5%; Score 897; DB 1; Length 784;
 CC Best Local Similarity 46.3%; Pred No. 4,60e-150;
 CC Matches 132; Conservative 83; Mismatches 72; Indels 20; Gaps 14;
 CC -----
 CC Db 63 ORKVFYTDAYDASQTTTLTVHVPVPLSVLEGNCIFAYGCTGCTKFTWGVGN 122
 CC Qy 65 DRSYVFDKNAPNVARQEDFDGLGVPLLDNAFKNCFIAYGCTGCKSYSMGWY-GK 123
 CC -----
 CC Db 123 DELMGITPTFEQWLIHN--RTE-NFOELVDVSYLEYMEELRLDKPNSK-HLEVYER 178
 CC Qy 124 EHT--GVIPRICQDFRINELQKDKNLCTCTVEYLEYINERVRLNLPSTKGNKVREH 181
 CC -----
 CC Db 179 -GSGTVVPLNHLAINKSVEDMIKVQGNKNTYGTGTMMNEHSSSHAFIMKI-EM-CD 235
 CC Qy 182 PSTGPVVEDIAKLIVRSFOETENLMDENSKARTVAATNMNTSSRSHAVFTLTQKH 241
 CC Db 236 TET--WTIKVGNLIDLAGSERQSKTGASAEKRLKASKINLAUGSSIGNVISALAE-SS- 291
 CC Qy 242 EHTMOTKVKALISVLDAGSRATSTGATGRULGASINSLSTUGRVIALADSSG 301
 CC Db 292 P---H-VPRDSKITLLOQSLGGNKTMTMNGPSKYNKNTLTLRYGSAKSN 346
 CC Qy 302 KQKKNLVPYRDSVLTWLLKSLGGSNTMTAIAISPANFEEETLSLTLYADSAKRKN 361
 CC Db 347 QPKNEDPDQAKLKEVQEIETRLK-RL 372

Oy 362 HAVNEDPNARMIRELBELAQLRSKL 388

RESULT 14

ID FL10_CHLRE STANDARD; PRT; 786 AA.

AC P48669;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

GN KINESIN-LIKE PROTEIN FLA10 (KHP1 PROTEIN).

GN FLA10.

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.

AW [1]

RP SEQUENCE FROM N.A.

RC STRAIN-137;

RA MEDLINE; 94299638.

RA Walther Z., Vashishtha M., Hall J.L.;

RT "The Chlamydomonas FLA10 gene encodes a novel kinesin-homologous protein."

AL J. Cell Biol. 126:175-188(1994).

CC - FUNCTION: PROBABLY INVOLVED IN FLAGELLAR ASSEMBLY AND MAINTENANCE.

CC - MAY PLAY A ROLE IN FLAGELLAR SYNTHESIS.

CC - TISSUE SPECIFICITY: FLAGELLAR AXONEME.

CC - SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.

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CC EMBL: L33697; AAA21738.1;

DR HSSP; P17119; 3KAE.

DR PFAM: PF00225; kinesin.1.

DR PRINTS: P00380; KINESINHEAVY.

DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.

DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.

KW Motor protein; Microtubules; ATP-binding; Coiled coil (BY SIMILARITY).

FT DOMAIN 1 358 MECHANOCHEMICAL (MOTOR).

FT DOMAIN 367 687 COILED COIL (POTENTIAL).

FT DOMAIN 688 786 GLOBULAR (POTENTIAL).

FT NP_BIND 97 104 ATP (POTENTIAL).

FT DOMAIN 388 391 POLY-GLY.

FT DOMAIN 705 714 POLY-GLY.

FT DOMAIN 756 759 POLY-ASP.

FT SEQUENCE 786 AA; 86671 MW; F90569203EB79F1B CRC64;

Query Match 16.0%; Score 870; DB 1; Length 786;

Best local similarity 40.0%; Pred. no. 1,84e-144;

Matches 187; Conservative 105; Mismatches 138; Indels 38; Gaps 22;

Db 6 GGSEVKKVYKRCPLNGKCAKDRSRVDMD---V-DA--G-GVKNRPNKADASEPPKA 57

Oy 2 SGGGNKIKVVRVFNAREIDRGAICVRNMGNTILTTPPGAENKARKSGKTMDGPKA 61

Db 58 FTFDQV---DWNCOQ--R--DVDFDITARLIDSCIEGYNGTIFAYGTGTGKSHTMEG- 109

Oy 62 FAFDRSYNSFDKNAPVARQEDLFDGLGVLLDNAPKNGYNCCIFAYGTGSGKSYSMWY 121

Db 110 KDSPPPELAGLIPNTRVYFIIATDSCTKEFIVRSYVLEIYNEVRDLNLDGHSKMKEL 169

Oy 122 GKRGVPIRQCQMFRRINEL-QKDKNLT-CTVEVSYLEIYNEVRDLNLTSPKGLKVR 179

Db 170 ESPDRGVYVDLSOFVCKNYENKMLVLAGKDNQGVGATLMQDNSSRHSFTTTECIE 229

Oy 180 EHGSTGPVVEDLAKLVRSQEIENLMDEGNKARTVAATNMNETSSRSRAVFTLTL--TQ 237

Db 230 KLESASAAKCFKAKODSNHVRVKNGLNVLDIAGSERQDKTGATGDRLEKIGINLSLTALG 289

Oy 238 KWHDE--E---TKMD-TE--KVAKISIVDLAGSERATSTGATCARLKEGAENRSLTLC 289

Db 290 NVISALVD---GK--SGH--IPYRDSKFLRLLODSLGGNTKTVVNIAGPADNNDTMTST 343

Oy 290 RYTAALADAMSSGKKNLQVPYRDSVLTWLLKDSIGGNSMTAIAALSPADINEETLST 349

Db 344 LRYANRAKNQKPNEDPKDAMLQRQBEIKLKBQLAARAAGGGGT-TM-PSGGGS 401

Oy 350 LRYADSAKRIRKNHVVNEDPNARMIRELBELAQLRSKLQSSGGGGGAGSGGPGVEESY 409

Db 402 FTKQIVR--TEEYDPIIDAIAQAMRAELEAKMK--SDISTEALDKAREE 447

Oy 410 PPTPLERQVSIQOPDATVKKRKAETVQLNQSEKLYRLDNLQTWEE 457

RESULT 15

ID KIF4_MOUSE STANDARD; PRT; 1231 AA.

AC P33174;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE KINESIN-LIKE PROTEIN KIF4.

GN KIF4 OR KNS4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AW [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ICR; TISSUE-BRAIN;

RA MEDLINE; 95014709.

RA Sekine Y., Okada Y., Noda Y., Kondo S., Aizawa H., Takemura R., Hirokawa N.;

RT "A novel microtubule-based motor protein (Kif4) for organelle transport, whose expression is regulated developmentally."

RT J. Cell Biol. 127:187-201(1994).

RL SEQUENCE OF 91-240 FROM N.A.

RP TISSUE-BRAIN;

RA MEDLINE; 91077686.

RA Aizawa H. Sekine Y., Takemura R., Zhang Z., Nangaku M., Hirokawa N.

RT "Kinesin family in murine central nervous system."

RL J. Cell Biol. 119:1287-1295(1992).

CC - FUNCTION: THE KINESIN FAMILY MAY RECOGNIZE, TRANSPORT AND POSITION THEIR SPECIFIC CARGOES IN A SINGLE TYPE OF NEURONAL CELL.

CC - TISSUE SPECIFICITY: EXPRESSED IN ADULT SPIREN AND JUVENILE BRAIN.

CC - SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.

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CC EMBL: D12646; BAA02167.1;

DR PIR: D44259; D44259.

DR HSSP; P17119; 3KAE.

DR MGD; MGI:108389; KIF4.

DR PFAM: PF00225; kinesin.1.

DR PRINTS: P00380; KINESINHEAVY.

DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.

DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.

KW Motor protein; Microtubules; ATP-binding; Coiled coil (BY SIMILARITY).

FT DOMAIN 1 350 MECHANOCHEMICAL (MOTOR).

FT DOMAIN 351 1000 COILED COIL (BY SIMILARITY).

FT DOMAIN 1001 1231 GLOBULAR.

FT NP_BIND 88 95 ATP (POTENTIAL).

FT CONFLICT 112 112 I -> S (IN REF. 2).

FT SEQUENCE 1231 AA; 139551 MW; F34F2C2D21158FE4 CRC64;

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(TM)

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	2215	40.9	1770	11	092119			KF1B-BETA.	0.00e+00
2	2051	37.8	1103	4	075186			KRAA0706 PROTEIN	0.00e+00
3	2051	37.8	1103	4	075186			KRAA0706 PROTEIN	0.00e+00
4	1976	36.4	1594	15	013778			CERINANE-14 KIN	0.00e+00
5	1858	34.3	1836	11	09W65			KF1B MAJOR ISOFORM	0.00e+00
6	1849	34.1	689	11	08B658			KINESIN-LIKE PROTEIN K	0.00e+00
7	1597	29.5	1921	5	001349			KINESIN-73.	1.37e-30
8	1308	24.1	1648	4	015038			KRAA0042 PROTEIN.	9.45e-23
9	1291	23.8	928	5	005997			PUTATIVE KINESIN-LIKE	3.96e-23
10	1258	21.7	1702	3	090867			KINASE PAM155 MEMBR	1.98e-18
11	954	17.7	1702	3	090867			KINASE PAM155 MEMBR	1.98e-18
12	904	16.7	744	13	093478			KINESIN-LIKE PROTEIN 3	2.57e-15
13	857	15.8	1121	5	019389			KINESIN-LIKE PROTEIN 3	1.71e-14
14	857	15.8	1121	5	020230			KINESIN-LIKE PROTEIN A	1.71e-14
15	854	15.8	1121	5	016866			KINESIN-LIKE PROTEIN A	7.23e-14
16	850	15.7	1121	5	019390			CHROMATIN ASSOCIATED K	4.94e-14
17	822	15.2	152	4	095654			KIF3 (FRAGMENT)	3.36e-13
18	822	15.2	152	4	095654			KIF3 (FRAGMENT)	3.36e-13
19	825	15.2	1226	13	091784			KINESIN-LIKE PROTEIN 1	7.98e-13
20	795	14.7	929	3	078718			KINESIN.	8.54e-13

[illegible]

Db 167 VREHPTLPGYVDLSSKLVTSYADIALMDGCKGKARTVAATNMNKTSSRSHAVFTIVFTQ 226
 QY 176 VREHPTLPGYVDLSSKLVTSYADIALMDGCKGKARTVAATNMNKTSSRSHAVFTIVFTQ 237
 Db 227 RSHDOLGLOSEKVKISLVNLAGERRADSGARCMRIKEGANINKSLTTLGKIVSIALAD 286
 QY 238 KWHDEPTKMDYKAVKISLVNLAGERRADSGARCMRIKEGANINKSLTTLGKIVSIALAD 297
 Db 287 LOS-KKKKSDPTVDSVSLVLLKLNKGNSTMTAALSPADINFEETLSLTKYADRTK 345
 QY 298 MSSGAQKKQLVPPVDSVSLVLLKLNKGNSTMTAALSPADINFEETLSLTKYADRTK 357
 Db 346 QIRCNVYINEDPNARILRELQREVARILRELLMAOGLSASALGLKVEGSPGVLPASS 405
 QY 358 RIKNHAVNEDPNARIMRELKELAEOLRSKL--QS-SGGG--PVEES 408
 Db 406 PPAPASPSPPHNGELSPSPAPQIGPEAMERLOETETIAELNETWEKLRKE 465
 QY 409 YP-PDPLKQIVSIO-OPD-A-TVR-KMSKAVIEQLNQSEKLYRDNLNWEKLAKE 463
 Db 466 ALMEREALALAMGSPGCHRTVGFSPKTPHLVNLNEDPLMSCLLYHKGVRVGV 525
 QY 464 EHKERAMALELGISIEKGFVGTIKEMPHLVNLSDDPLACLVTNFKGQTRGVN 523
 Db 526 --DV--DIKLGQFIREQGLFRSIPQPGETWVTLPECEGAETYNKLYTEPLVLSG 581
 QY 524 NQDTQAEIRLNGSKLKECHTENV--D-NV-VTVPNKAAVNGVRIKDPTRLRSG 578
 Db 582 NRIVYMGKHNVRNHPHPCARLRE 605
 QY 579 YRIILQDFHIFRHNHPEARAQ 602

RESULT 4
 AC Q18798 PRELIMINARY; PRT: 1584 AA.
 ID Q18778;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 GN UNK-104 KINESIN-LIKE PROTEIN (PIR:J0114).
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 RN Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 [1]
 RX MEDLINE; 94150718.
 RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONFIELD J., CONNELL M., COPSEY T., COOPER J., CRAXTON M., DEAR S.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSON L.,
 RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WILKINSON-SPOAT J., WILKINSON-SPOAT J., WILKINSON-SPOAT J.,
 RT *23486; contiguous nucleotide sequence from chromosome III of C.
 RL Nature 368:32-38(1994).
 [2]
 RN SEQUENCE FROM N.A.
 DU 2;
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; 050135; AAA93453.1;
 DR HSP; PJ1119; 3KAR.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAINI; 1.
 DR PFAM; PF00225; kinesin.1.
 DR PFAM; PF00169; PH; 1.

DR PRINTS; PRO0380; KINESINHAVT.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 SQ SEQUENCE 1584 AA; 75BE1D7D CRC32:
 Query Match 36.4%; Score 1971; DB 5; Length 1584;
 Best Local Similarity 52.6%; Pred. No. 0.00e+00;
 Matches 318; Conservative 12; Mismatches 127; Indels 38; Gaps 20;
 Db 2 SVYVAVYRPNREISWTSKVLQVNGNTTIN--G--HSINKE-N-F-----SPNF 49
 QY 5 GNIVYVYRPNREISWTSKVLQVNGNTTIN--G--HSINKE-N-F-----SPNF 49
 Db 50 DRYVSFARNDEHPTKQYVLELVGHPAGYNNCFAYGTCGSKGYTMGKAF 64
 QY 65 DRYVSFARNDEHPTKQYVLELVGHPAGYNNCFAYGTCGSKGYTMGKAF 64
 Db 110 DRYVSFARNDEHPTKQYVLELVGHPAGYNNCFAYGTCGSKGYTMGKAF 122
 QY 123 KEB-GVPRICODMFRINELQKDKLCTCTVSVLEIYNVROLNLPSTGNKLVREH 181
 Db 169 PLUGPYVDLTKMAVSYHDTCLMDGKARTVAATNMNKTSSRSHAVFTIVFTQ 228
 QY 182 PSTGPTVEDLAKLVVRSFOEINLMDGKARTVAATNMNKTSSRSHAVFTIVFTQ 241
 Db 229 ADSNLTQKHSKISLVLAGSRANSGARCMRIKEGANINKSLTTLGKIVSIALAD 288
 QY 242 EHKERAMALELGISIEKGFVGTIKEMPHLVNLSDDPLACLVTNFKGQTRGVN 301
 Db 289 KKSNGKGVIPVDSVSLVLLKLNKGNSTMTAALSPADINFEETLSLTKYADRTK 348
 QY 302 KQKNG-LVPYRDSVSLVLLKLNKGNSTMTAALSPADINFEETLSLTKYADRTK 360
 Db 349 QAVYVNDPNAKLRELNEEVIKRHLKDKG----IDVTD--VOET--PGR--HKK-G 396
 QY 361 NHAVYVNDPNAKLRELNEEVIKRHLKDKG----IDVTD--VOET--PGR--HKK-G 396
 Db 397 P-KLP-AHVH----EOL-EKLOSEKLMKEIKRTWOKLHTEERKQREELRDMGLAC 449
 QY 421 STQOQPTVKKMSKAIEVDSQUNSEKLYRDNLNWEKLAKEEIKEREAALELGIS- 479
 Db 450 AEDCTTLGVSFKPLPHLVNLSDDPLACLVTNFKGQTRGVN 509
 QY 480 TEKGF-VQYHSEKPHLVNLSDDPLACLVTNFKGQTRGVN 538
 Db 510 LELHCFINEDGNVTLTKMKNPACSYNGKQVTPVTLHGTSRVILGPHHVRVNDQEAR 569
 QY 539 LKHECTFENVVTVIYPNEKAAVNGVRIKDPTRLRSGYRIILGDFHIFRHNHPEAR 598
 Db 570 QSRHN 574
 QY 599 AEROE 603

RESULT 5
 ID Q9WVES; PRELIMINARY; PRT: 1816 AA.
 AC Q9WVES;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 GN KIF1B MAJOR ISOFORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Butleria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RA CONFORTI L., BUCKMASTER A., TRAILTON A., BROWN M.C., LYON M.F.,
 RA PERRY V.H., COLEMAN M.P.;
 RT "The major brain isoform of Kif1b lacks the putative mitochondria-
 RL binding domain.";
 RL Mamm. Genome 10:0-0(1999).
 DR EMBL; AF131865; AAD39438.1; -.

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DR      FFAM; FF01302; CAP_GLI; 1.
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[illegible]

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Db 1 MKGDSIIIVAVRVPFNDREKTRNCKLVIEIMPDETTIVIRDPKTNDEKRTYDHSYV-SH 59
Oy 1 MSGGGNIKVVRVPFNAREIDRGAKCIVRM-EGNOTILTTPPGAEEKARKSGKTMDCP 59
Db 60 DGFS-EKNGVLEPTDPHYADQRVFEEDLGRGVLANAWAGYSCLEFAYGOTGSGKSYSTV 118
Oy 60 KAFADRSYWSFKAPNAPYARQEDFQDLGVPLLDNAFKYNNCFAYGOTGSGKSYNM 119
Db 119 GFKNNGKIVPTICEELFKQIAD-NKKNNQMFVFFVSMYEIYCEKVRDILLSSTPPPGGLK 177
Oy 120 GYKGEVGPRIQCDMFRINELQDKNLTCVTEVSYLEYINERVROLLN--PSTKGNLK 177
Db 178 VREHPKNGFVNLVTPVNSFKTEAKIEBETSKRTSIATATOMATSSRAHTIVKTFNQ 237
Oy 178 VREHPSTGYFVEDLAKLVFSQFETENLMDGNKARVATNMNETSSRHAVFTLTQ 237
Db 238 KSKQAGGTSMKK-SEINLVLDLAGSRQSAAGTEGDRLEKEGIVINQSLTGLGRVIALHD 296
Oy 238 KWIDEETKMDTEKVAKISLVLDLAGSERATSTGATGARKEGAEINRSLTGLRVIALAD 297
Db 297 SOKASGKQTOIPYRDSVLTCLLKALNGSKNSTIMIAISPADINFEETLSTLRFADRAK 356
Oy 298 MSSGKQKNOLVYRDSVLTLLKDSLGNSNTAMIAATSPADINFEETLSTLRYADSAK 357
Db 357 SIKTNVAVNENOTERALRELRENLRLOSIOGGTAGDAS 396
Oy 358 RIKNHAVNEDPNARMIRELKELAQLRSKLGSSGGGGG 397
RESULT 10
ID Q20888 PRELIMINARY; PRT: 1576 AA.
AC Q20888
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE SIMILAR TO KINESIN-RELATED PROTEIN. NCBI GI: 1109842.
GN F6653.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94130618;
PA WILSON, J., ALSCOGGH, R., ANDERSON, K., BAYNES, C., BERKS, M.,
PA BONFIELD, J., BURTON, J., CONNELLEY, R., COOPER, J., COULSON, A.,
PA CRAXTON, M., DEAR, S., DI, J., FAVELLO, A., HUTTON, L.,
PA GARDNER, A., GREEN, P., HAKINS, T., HALLER, L., JERRE, M., JOHNSON, L.,
PA JONES, M., KERSHAN, J., KIRSTEN, J., LAISER, L., LATREILLE, C.,
PA LIGHTNING, J., LLOYD, C., MCUREAY, A., MORTIMORE, C., O'CALLAHAN, M.,
PA PARSONS, J., PERCY, C., RIEKEN, L., ROOPA, A., SAUNDERS, D., SHOWNKEEN, R.,
PA SMAILDON, N., SMITH, A., SONNENHAMMER, E., STADEN, R.,
PA THIERRY-MIEG, J., THOMAS, K., VAUDIN, M., VAUGHAN, K., WATKINSON, R.,
PA WATSON, A., WEINSTOCK, L., WILKINSON-SPOFF, J., WOULDMAN, P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans*.
RL Nature 368:32-38(1994).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA GATTUNG, S., WU, X.;
RN Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

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RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DB EMBL; U41536; AAB52613.1;
DR HSP; P33176; I962.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PFAM; PF00225; kinesin; 2.
DR PRINTS; PR00380; KINESINHEAVY.
KW Motor protein; Microtubules; ATP-binding; Colled coil.
SQ SEQUENCE 1576 AA; 177409 MW; 80015D5C CRC32;
Query Match 50.7%; Score 1124; DB 5; Length 1576;
Best Local Similarity 54.5%; Pred. No. 1.18e-199;
Matches 225; Conservative 65; Mismatches 78; Indels 45; Gaps 19;
Db 8 SAVKVAIRVRFNFKRELDLTKSVYRQKQCVL-HHP-IEEK--NS-KT-----FTF 55
Oy 5 GNIKVVVRVRFNAREIDRGAKCIVRMENQNTLTPPGAEEKARKSGKTMDCPKAF 64
Db 56 DRHGFSTDPHSYDFASQSTVSYHLGSGVVENAFSGNACIFAYGOTGSGKSYVTWMTQD 115
Oy 65 DRSYWSFKAPNAPYARQEDFQDLGVPLLDNAFKYNNCFAYGOTGSGKSYSMGYKE 124
Db 116 PGIIPRVCDNLETRIQE-TSGNSLSFKVEYSMEIYNERVROLLDPKSKKALKVREHKI 174
Oy 125 HGVIPIRQCDMFRINELQDKNLTCVTEVSYLEYINERVROLLNPNSTGN-LKVRHPS 183
Db 175 LGPWVDGLSLVANSFEQISNLLLEGNNKSRVTAATNMNAESSRSRHAVFTLTLDLHLE 234
Oy 184 TGPYVEDLAKLVVRSFQEIENLMDGNKARTVAATNMNETSSRHAVFTLTLOKHDEE 243
Db 235 NGTSGSEKVAKISLVLDLAGSERATSTGATGARKEGAEINRSL-ST-----G-R-- 290
Oy 244 TKMDTEKVAKISLVLDLAGSERATSTGATGARKEGAEINRSL-ST-----G-R-- 290
Db 295 ADYVVEINQKIDFRSLTFLQWISALAEARNKSKDKFTIPYRDSVLTLLKDSIGGNSRTVM 354
Oy 291 ----V-IA-----ALA--DM--SS-G-KQ-KKNOLVYRDSVLTLLKDSIGGNSHTAM 332
Db 355 IATLSPADNAYEETLSTLRYADRAKKIVNHAIINEDPNARVIRELEVETLR 407
Oy 333 IATLSPADINFEETLSTLRYADSAKRKNHIAVNVNEDPNARMIRELKELAQLR 385
RESULT 11
ID Q94496 PRELIMINARY; PRT: 702 AA.
AC Q94496
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE KINESIN FAMILY MEMBER PROTEIN KIF3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1].
RP SEQUENCE FROM N.A.
RC TISSUE-RETINA;
RA BURNSTEIN, B., BOST-USERING, L., HOANG, E., FRAZER, K.A., REICHEL, S.,
RA SUBMITTED (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; F504183; AAC72924.1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
KW Motor protein; Microtubules; ATP-binding; Colled coil.
SQ SEQUENCE 702 AA; 80337 MW; 35968AD6 CRC32;
Query Match 17.7%; Score 958; DB 4; Length 702;
Best Local Similarity 40.8%; Pred. No. 1.22e-164;
Matches 193; Conservative 107; Mismatches 136; Indels 35; Gaps 27;
Db 14 NVKVVVRVRFNAREIDRGAKCIVRMENQNTLTPPGAEEKARKSGKTMDCPKAF 64

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QY 6 NIKVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEKARKSGKTIIDGPKAFPD 65
Db 65 -T--VF---GPE-SKOLDVY-NLTARITDSVLEGNGTIFATGQTGKTIEMGVRAI 116
QY 66 RSTWFSFKNAPYAROEFDQDGLV-PLDNPAGKYNCFIATGQTGSKSYMMGT-GK 123
Db 117 PELRGITPNSFAHIFGHIAKACDTRPL--VRYVSYLEYNEVDRLJGCKOORLAYKER 174
QY 124 -E-HVGIPIQDFNFRINELQKUNLCTCTVYSVLEITNRYVDLLNPSTGKNLAYKREH 181
Db 175 PDGVGYIKOLSAVYNNADMDORTLCHKWRSYGATNKNHSSSRSHAITITITCEKSG 234
QY 182 PSTGPVEDLAKLVPSFQIEIWLMDGSKARTVAATNMNETSSRSHAVFTLTLOKWH 241
Db 235 IDGNMHV-RMGLKHLVDLAGSERQATGCRLEKATKINLSLTGLMGVIALVD---G 290
QY 242 EETKMDTEVKATISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALDMSG 301
Db 291 K--STH--VPYRNSKTRLLQDSIGSKTMCANIGPADYNTDETISTRYANRKNIKN 347
QY 302 KQKKNLQVLPYRDSVPLMLKDSIGSKTMCANIGPADYNTDETISTRYANRKNIKN 361
Db 348 KARINEDPKALLPQKRETELEKKLLEP-GEIEGSDISGEEDDEEGEVEDGEKRR 406
QY 362 HAYVEDPNAIRNELKELELAQSKLSGSGGGGAGGSGGPVEESTPTPTPEKIOYVS 421
Db 407 KREIOICKKVSPDKIE-W-QA-KIDPE-RKALETKLDMEEFERKARELE 455
QY 422 IQQPDATVKKMSKAETVPLQNLSEKLYRDLNQTWEELAKTEETHKEREAALE 474

RESULT 12
ID 093478 PRELIMINARY: PRT: 744 AA.
AC 093478;
DT 01-JAN-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE KINESIN LIKE PROTEIN 3.
GN XLIP3.
GC Xenopus laevis (African clawed frog).
OC Actinoptera; Actinoptera; Chordata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93246065.
RA VERNOS J., HEASMAN J., WYLIE C.;
RT "Multiple kinesin-like transcripts in Xenopus oocytes.";
RL Dev. Biol. 157:232-239(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA LE BOT N., ANTONY C., WHITE J., KARSENTI E., VERNOS J.;
RT "Role of Xk1p3, a subunit of Xenopus kinesin II heterotrimeric
complex, in membrane transport at the ER/Golgi interface.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBD databases.
DE EMBL: AJ008639; CA008879.1; -.
DR EMBL: AF002054.1; KINESIN_MOTOR_DOMAIN1; 1.
DR PRINTS: PR00340; KINESINHEAVY.
KW Motor protein; Microtubules; ATP-binding; Coiled coil.
SQ SEQUENCE 744 AA; 84873 MW; 5674E1D1 CRC32;

Query Match 16.78; Score 904; DB 13; Length 744;
Best Local Similarity 46.5%; Pred. No. 2.57e-153;
Matches 155; Conservative 72; Mismatches 92; Indels 14; Gaps 9;

Db 53 LSKTF-TFVATSDNSKVOLEYVETFRPLVDVLLGNGTIFATGQTGKTIEMGVRAI 111
QY 64 FDRSTWFSFKNAPYAROEFDQDGLVPLDNPAGKYNCFIATGQTGSKSYMMGT-G 122
Db 112 DPEKRGVPSFEHIFTHISRSQNOYL---VRASYLEYQETIRQLLSKDKSRLEAKE 168
QY 123 K-E-HVGIPIQDFNFRINELQKUNLCTCTVYSVLEITNRYVDLLNPSTGKNLAYKRE 180

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Db 169 RPDIGVYKOLDSFVYSKVEIEHVVNNGVGNRSGVATNMNHESSSRSHAITPITI--ECSQ 227
QY 181 HFSTGPYVEDLAKLVPSFQIEIWLMDGSKARTVAATNMNETSSRSHAVFTLTLOKWH 240
Db 228 IGLDGENIRVGLKMLVDLAGSERQTKTGAQGERLKEATKINLSLALGNVISALVD--- 284
QY 241 DEETKMDTEVKATISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALDMSG 300
Db 285 GR--STH--IPYRNSKTRLLQDSIGSKTMCANIGPADYNTDETISTRYANRKNIKN 341
QY 301 GAKKKNLQVLPYRDSVPLMLKDSIGSKTMCANIGPADYNTDETISTRYANRKNIKN 360
Db 342 NKPRVNEPDKALLPQKRETELEKKLLEP-GEIEGSDISGEEDDEEGEVEDGEKRR 406
QY 361 NHAVVEDPNAIRNELKELELAQSKLSGSGGGGAGGSGGPVEESTPTPTPEKIOYVS 421

RESULT 13
ID 018389 PRELIMINARY: PRT: 1121 AA.
AC 018389;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE KINESIN-LIKE PROTEIN, KUP388.
GC Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97296456.
RA OHKURA H., TOROK T., TICK G., HOHEISEL J., KISS I., GLOVER D.M.;
RT "Mutation of a gene for a Drosophila kinesin-like protein, Klp388,
leads to failure of cytokinesis.";
RL J. Cell Sci. 110:945-954(1997).
DR EMBL: Y10667; CAAT1675.1; -.
DR HSPB: P17119; 3KAN.
DR FYBASE: FBgn0004374; neb.
DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PIR: P00428; KIN.
DR PRINTS: PR00380; KINESINHEAVY.
KW Motor protein; Microtubules; ATP-binding; Coiled coil.
SQ SEQUENCE 1121 AA; 125194 MW; B0A069F6 CRC32;

Query Match 15.88; Score 857; DB 5; Length 1121;
Best Local Similarity 37.3%; Pred. No. 1.71e-143;
Matches 243; Conservative 147; Mismatches 179; Indels 83; Gaps 42;

Db 115 VSEESNIVAVRPLNALECTRGQTVNYYVHGNSNELTVQAGSADAS-AG--VTH-- 169
QY 1 MSGGGKIVVVRFPNAREIDRGAKCIVRMEGNOTILTPPGAEKARKSGKTIIDGPK 59
Db 170 -FFSYQVYVSCDPERKNFCAQKVPETARPLIDTAFEGYNACLFAYGQTGSKSYMM 228
QY 60 KAFAPDRSTWFSFKNAPYAROEFDQDGLVPLDNPAGKYNCFIATGQTGSKSYMM 119
Db 229 GTEALDDAALDGGPHDEAGIIPRECHLEPREIAKVSQOOLQVEVSEVSEYETNEK 288
QY 120 GY-G--K--E---H---GVIPRICQDFRINELQKUNLCTCTVYSVLEITNRYVD 166
Db 289 LLSVQVHAATAGESTPTQQQQQOORPALKVREHPITGPPYVDLSAHSVDSYALRN 348
QY 167 LL---NPST-KGN-----LKVREHPSTGPPVEDLAKLVRSFOEINLMD 208
Db 349 GNSORATATAAMDKSSRSRSHIFNVLNMLDLSSDDGLSDSDSTASSLROTFRHS 408
QY 209 GNKARTVAATNMNETSSRSHAVFT--LTLTQ--KWHO---E-ETKNOTE-K-V--AK 256
Db 409 VDLAGSERISYNGSERIREGVSINSLTLGKYVIAALDASRKASANGPLGSGTPTFV 468
QY 257 VDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALD---MSSG-Q--K-K-N 309

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[illegible]

DB	690	IEHGGKLYIPGSEDFETYVNGELLKDRRLFHGDRLVGGSHYFRISNP	741
QY	545	FENV-DNVVTTVP-NEKAAVMVGVRIIDKPTRLRSGVRIILGDFHIFRFNHP	594

Query Match 15.8%; Score 854; DB 5; Length 1121;
Best Local Similarity 37.3%; Pred. No. 7.23e-143;
Matches 243; Conservative 146; Mismatches 180; Indels 8
SEQUENCE 1121 AA; 125236 MW; A43A76BF CRC32;

[illegible]

Oy 209 GKARTVAATNNNETSRSHAVFT--LTLQ-KHID---E-ETKMQTE-K-V--AKISL 256
Db 409 VDLASERISVSGNGERTREGYSINKSLTLGKVIAAALADSKAIANGPIGSGTPTFTV 468
Oy 257 VDLASERATSTGATGARLKGAENRSLTLGRVIAALAD---MSGKQ-K-K-NOLV 309
Db 469 PTRESVLTWLLRENLGGNGKTYMLATISPASTHADETATLRYACKARSIYVRKYVNESP 528
Oy 310 PTROSVLTWLLKDSLGGNSMTJAAIAPADINFEETLSTLRADSKRKIRKHAVYNEDP 369
Db 529 HDKTIROLRAEVDRLKS-LRNEXYERORL--SGNS-NNEVPKRIIET---SVDETE--V 579
Oy 370 NARMIRELKEELAQLRSKLQSSGGGGGAGGGGPPDEPLEKQIVSIQPPDATV 429
Db 580 EAL-ROQLAER--ERE-LSRA-QKSMWEKLEADQKSELRLVLRRLGLE--LTAE-Q 631
Oy 430 KMSKAEIVQOLNOSKLYRDINOTWEEKLAKTEIHKEREAALEELGTSIEKFGVGYH 489
Db 632 -KO-ACLVNLTADPILSGTLFVLLPQGLVRIGRGLPGSSSSQPDIVLDGPLVALQHS 689
Oy 490 SKEMPHVNLSDOPLAACLIVNIKPGQTRVG-N-V---NODTOAERLNGSKILKEHCT 544
Db 690 IEHERGKLYVIGSEDFETVNGELLKDRQLFHGDRLVIGGSHYFRISNP 741
Oy 545 FENV-DNVVTIVP-NERAAVWNGYRIDKPTRLASGYRIILGDPHIFRNP 594

Search completed: Mon Aug 21 15:42:14 2000
Job time : 66 secs.

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MPARLH (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Aug 21 15:42:31 2000; MacPar time 15.62 Seconds
Tabular output not generated. 724.633 Million cell updates/sec

Title: >US-09-235-416-1
Description: (1-784) from US09235416A.pep
Perfect Score: 5422
Sequence: 1 MSGGNIKVVVRFPNARE.....ELRQQQAQMEALKTAQEF 784
Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: 1:US-COMB 2:5B-COMB 3:6-COMB 4:PCT-COMB 5:backfiles1
Statistics: Mean 35.470; Variance 183.982; scale 0.193

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2037	37.6	1103	3	US-09-162-373-1	1.07e-153
2	953	17.6	952	4	PCT-US94-0	Sequence 1, Applicatio 7.47e-95
3	953	17.6	952	4	US-08-933-	Sequence 3, Applicatio 7.47e-95
4	953	17.6	952	4	US-08-933-	Sequence 3, Applicatio 7.47e-95
5	953	17.6	952	4	US-08-933-	Sequence 3, Applicatio 7.47e-95
6	707	13.6	411	2	US-08-713-	Sequence 3, Applicatio 5.23e-45
7	707	13.6	411	2	US-08-713-	Sequence 3, Applicatio 5.23e-45
8	196	3.6	1612	3	PCT-US94-0	Sequence 48, Applicati 2.01e-05
9	196	3.6	1612	3	US-08-545-	Sequence 2, Applicati 2.01e-05
10	120	2.2	1354	2	US-08-685-	Sequence 2, Applicatio 2.95e-00
11	101	1.9	594	4	PCT-US94-1	Sequence 6, Applicatio 4.45e-01
12	95	1.8	240	4	US-08-362-	Sequence 30, Applicati 1.01e-02
13	95	1.8	240	4	US-08-362-	Sequence 30, Applicati 1.01e-02
14	95	1.8	240	4	US-08-362-	Sequence 30, Applicati 1.01e-02
15	98	1.8	274	2	US-08-860-	Sequence 12, Applicati 6.74e-01
16	97	1.8	280	2	US-08-403-	Sequence 10, Applicati 5.12e-01
17	100	1.8	371	4	US-08-432-	Sequence 76, Applicati 1.01e-02
18	95	1.8	414	4	PCT-US91-0	Sequence 2, Applicatio 1.01e-02
19	95	1.8	414	4	PCT-US91-0	Sequence 2, Applicatio 1.01e-02
20	95	1.8	414	4	PCT-US91-0	Sequence 2, Applicatio 1.01e-02
21	95	1.8	414	4	PCT-US91-0	Sequence 2, Applicatio 1.01e-02
22	95	1.8	414	4	PCT-US91-0	Sequence 2, Applicatio 1.01e-02
23	100	1.8	425	2	US-08-366-	Sequence 2, Applicatio 5.12e-01

24	100	1.8	442	2	US-08-687-	Sequence 6, Applicatio 5.12e-01
25	95	1.8	442	2	US-08-687-	Sequence 6, Applicatio 5.12e-01
26	96	1.8	470	2	US-08-933-	Sequence 3, Applicatio 8.85e-01
27	96	1.8	491	1	US-08-489-	Sequence 3, Applicatio 8.85e-01
28	96	1.8	491	1	US-08-489-	Sequence 3, Applicatio 8.85e-01
29	97	1.8	517	2	US-08-799-	Sequence 2, Applicatio 7.72e-01
30	97	1.8	566	2	US-08-533-	Sequence 8, Applicatio 7.72e-01
31	95	1.8	656	2	US-08-531-	Sequence 2, Applicatio 1.07e-01
32	95	1.8	656	2	US-08-531-	Sequence 2, Applicatio 1.07e-01
33	97	1.8	753	3	US-08-946-	Sequence 6, Applicatio 7.75e-01
34	96	1.8	753	3	US-08-946-	Sequence 6, Applicatio 7.75e-01
35	100	1.8	924	1	US-08-656-	Sequence 28, Applicati 5.12e-01
36	100	1.8	924	1	US-08-481-	Sequence 28, Applicati 5.12e-01
37	100	1.8	924	1	US-08-485-	Sequence 28, Applicati 5.12e-01
38	100	1.8	924	1	US-08-487-	Sequence 28, Applicati 5.12e-01
39	98	1.8	1093	4	PCT-US94-0	Sequence 55, Applicati 6.74e-01
40	98	1.8	1093	4	PCT-US94-0	Sequence 55, Applicati 6.74e-01
41	94	1.7	312	3	US-08-414-	Sequence 2, Applicatio 1.16e-02
42	93	1.7	368	2	US-08-856-	Sequence 4, Applicatio 1.33e-02
43	94	1.7	802	2	US-08-007-	Sequence 4, Applicatio 1.16e-02
44	92	1.7	876	4	PCT-US95-0	Sequence 34, Applicati 1.52e-02
45	92	1.7	876	4	PCT-US95-0	Sequence 32, Applicati 1.52e-02

ALIGNMENTS

RESULT 1	ID	US-09-162-373-1	STANDARD:	PRT:	1103 AA.
XX	AC	xxxxxx			
XX	DT				
XX	DE				
XX	DE				
XX	CC	Sequence 1, Application US/09162373			
CC	CC	Sequence 1, Application US/09162373			
CC	CC	Patent No. 6013454			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: Wang Y. Tom			
CC	CC	APPLICANT: Guebler, Karl J.			
CC	CC	APPLICANT: Patterson, Chandra			
CC	CC	TITLE OF INVENTION: KINESIN-LIKE MOTOR PROTEIN			
CC	CC	FILE REFERENCE: PF-0593 US			
CC	CC	CURRENT APPLICATION NUMBER: US/09/162.373			
CC	CC	CURRENT FILING DATE: 1998-09-28			
CC	CC	NUMBER OF SEQ ID NOS: 2			
CC	CC	SOFTWARE: PERL Program			
CC	CC	SEQ ID NO 1			
CC	CC	LENGTH: 1103			
CC	CC	TYPE: PRT			
CC	CC	ORGANISM: Homo sapiens			
CC	CC	FEATURE: 1281811			
CC	CC	OTHER INFORMATION: 1281811			
CC	CC	SEQUENCE 1103 AA, 122860 MW, 5804959 CN;			
CC	CC	Query Match 37.6%; Score 2037; DB 3; Length 1103;			
CC	CC	Best Local Similarity 54.2%; Pred. No. 1.07e-153;			
CC	CC	Mismatches 127; Indels 42; Gaps 28;			
CC	CC	Matches 339; Conservative 127; Mismatches 118; Indels 42; Gaps 28;			
DB	DB	1 MAGAS-VKVVAVRFPNARETSODAKCVSMOQNTSIINP-----K-Q-S-K---DAPK 48			
QY	QY	1 MSGGNIKVVVRFPNAREIDRGAKCVLMGEGNOTILTPPGAEKARKSKTINDGPK 60			
DB	DB	49 SFTDYSYWSHTSTEDPQAFQOQVTRDICEEMLLHAFEGYNVICFAYGOTGACKSYTM 108			
QY	QY	61 AFADKSGYSGF-DKNAENTARQEDFQDLVLLONAFKYNKNCIFAYGOTGCKSYTM 119			
DB	DB	109 GRQFGQGGIVPOLCEDLSFVSQNSQAQ-LSYSVFVSMYCYCERVRLDLPKNSGSLR 167			
QY	QY	120 G-YK-EGNVIPIQDQMPRIEQLQDKMLCTCVSEVLTENRVLNLPSTNGSLR 177			
DB	DB	168 VREHPIPLGVQDLSKLVTSYADIADLMOCGNKARTVAATNNETSSRHAFVTFQ 227			


```

CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98103
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple Macintosh Operating System 7.1
CC SOFTWARE: Microsoft Word for Macintosh 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/282,845
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/006,676
CC FILING DATE: JANUARY 15, 1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Perkins, Patricia Anne
CC REGISTRATION NUMBER: 34,693
CC REFERENCE/DOCKET NUMBER: 5004-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)387-0640
CC TELEFAX: (206)233-0643
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 955 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 955 AA; 106167 MW; 3654125 CN;

Query Match 17.6%; Score 953; DB 1; Length 955;
Best Local Similarity 43.5%; Pred. No. 7,47e-65;
Matches 177; Conservative 90; Mismatches 111; Indels 29; Gaps 18;

Dd 13 VKVSVVRPLNERENNAPEGTKVTVAAQAAAVYTKVIGSGNNSGAAESMGTARRVAQD 72
Qy 7 IKVVVRVPENAREID-R-GAKCIVR-MEGNOTI-LTPPGAEEKAKSGK-TIMDGPKA 61
Dd 73 FQFDHVFWSVETPDACGATPATQADVFRTIGYPLVQHAFDQFNSCLFAYGQTSGKTYTM 132
Qy 62 FAFDRSWSFEDK-NA-PNT-ABQEDLPQDGLVPLDPAFKYNNICFAYGQTSGKSYSM 118
Dd 133 MGADVSALSGEGNGVTPRICLEIFARKASVEAQGSHRWELGVEYVYNERVSDLLGRK 192
Qy 119 MG-----Y-GKHGVGIPRCQDMFRFRIQLQKDKNTCTVSVYLEYNERVDLI-NP- 170
Dd 193 KGWKGGEVEYVDVREHPSRGVYFLEG-ORLVEVSGSDVYRLIEISGVYRITASTKNDR 251
Qy 171 -STKG---NL--KYREHPSTGPYVEDLAKLV-VRSFQETENLMDENCKARTVAATNNET 223
Dd 252 SRSRSHAIMLLREERTMTKSGETIRTAGKSSRMNIVDLAGSERVAQSQVEGQFKEAT 311
Qy 224 SRSRSHAVFTLITQR-----HDEETKMDTEYKAKISLVPLAGSRATSTGATGARLKEGA 279
Dd 312 HINLSLTLGRVIDVLADMATKGAKAQSVAPFRFDKSLFTLIKDSLGGNSKTFMIATVSP 371
Qy 280 EINLSLTLGRVIAALADMS--GKQKNOLVPYRDSVLTWLLKDSLGGNSMTAMIAISP 338
Dd 372 SALNYETLSLTRYASRADRVINVAQVNBDPRRRIRLEBQMDMR 418
Qy 339 ADINFEETLSLRVADSAKKIKNHAVYVNDPDMARKRELKLELAQLR 385

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RESULT 6
ID US-08-713-815A-4 STANDARD; PRT; 411 AA.

Sequence 4, Application US/08713815A

```

XX Sequence 4, Application US/08713815A
CC Patent No. 5830659
CC GENERAL INFORMATION:
CC APPLICANT: Russell J. Stewart
CC TITLE OF INVENTION: ACTIVE MICROTUBULE-BASED
CC NUMBER OF INVENTION: SEPARATIONS BY KINESINS
CC NUMBER OF SEQUENCES:
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
CC COMPUTER: AST Ascentia 900N
CC OPERATING SYSTEM: DOS 6.22
CC SOFTWARE: Word Perfect 6.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/713.815A
CC FILING DATE: 13-SEP-1996
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Alan J. Howarth
CC REGISTRATION NUMBER: 36,553
CC REFERENCE/DOCKET NUMBER: T3214/0-2202
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 411 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 411 AA: 45925 MW: 836180 CN;

Query Match 13.0%; Score 707; DB 2: Length 411
Best Local Similarity 42.0%; Pred. No. 5,23e-45;
Matches 136; Conservative 77; Mismatches 91; Indels

Db 55 FDKVFPNASEKYNKAAKSVITDVLGVNGTIFPAGTGTSGKTKTHMEGVY
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 PRIVDNPENIYAM--EYNLEPHIKYKSYEYIMDKIRLDLVS-KVNLVS
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 IPRICDMPRLNELOKMLKTVSEYVSLIYINERVLNADFTGKLNKVR
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 VKGATERPSSPDVFEVIEKSKNRHIAITANNHSSHSUSVPLNLYKNE
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 VEDLAKLVRSFOEINLMDGKNKARIYAATNNKTSNHNPTLTLTQK
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 S---GKLYLDLAGEKSYTGAGCTVLDPAKNTKSLGKLVISALAD---
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 TEKVAKISLVLAGESEATSTGATGARKEGAEINRSLSTLGRVIAALADMS
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 283 -IPYROSKLTPILOESLGGNARTTIVCCSPASENSESTKSLDFGRKATV
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 LVPYRDSVLTLWLLKSLGNSMTAMIAISPADINPEETLSTLRVYADSAKRI
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 342 ELTAEEWRRRYKEKEKNARKLAKGVE 367
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 D--PNARMIR-EL-KEELAQLRASKLQ 389
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 7
ID US-08-713-815A-3
XX
AC xxxxxx
STANDARD; PRT; 441 AA.

XX DT

XX DE Sequence 3, Application US/08713815A
XX CC Sequence 3, Application US/08713815A
XX CC Patent No. 5830659
CC GENERAL INFORMATION:
CC APPLICANT: RUSSELL J. Stewart
CC TITLE OF INVENTION: ACTIVE SITE OF PROTEIN-BASED
CC TITLE OF INVENTION: SEPARATIONS BY KINESINS
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5830659th & Western, L.L.P.
CC STREET: 3035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
CC COMPUTER: AST Ascentia 900N
CC OPERATING SYSTEM: DOS 6.22
CC SOFTWARE: Word Perfect 6.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08713,815A
CC FILING DATE: 13-Sep-1996
CC CLASSIFICATION: 35
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Alan J. Howarth
CC REGISTRATION NUMBER: 36,553
CC REFERENCE/DOCKET NUMBER: T3214/U-2202
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 441 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 441 AA; 48936 MW; 924366 CN;
Query Match 13.08; Score 707; DB 2; Length 441;
Best Local Similarity 42.38; Pred. No. 5,238-45;
Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;
Db 55 FDKVFPKNSQKVKYNEAKSIVTDVLAGYNGTIFAYGQTSGSKTHTWGVGDSYKQGI 114
QY 71 FDKNAPYARQEDFDGLGVPLLDNAFKYNNCFAYGQTSGSKYSNMG-YGKE--HGV 127
Db 115 IPRVINDNIHYAM--EVNLEFHKIVSYRYIMDKIRDLIDVS-KVNLVSWEKDRVPY 171
QY 128 IPRICQMFRIINELOKQKULCTVEYSLEYTYNERVDRLLNPSTKGLKLVREHPSTGPY 187
Db 172 VKGATERVSSPEDVFVEIECKSNRIHAYVNNNHSRSKSHVELINYKQENLEKQKL- 230
QY 186 VEDLAKLVRSFDEINLDEGNKARTVAANNNETSSSHAVFTLTQKHDEETKMD 247
Db 231 S--GKIVLVLAGSKVSTGAGVLDKAKINKSLGALGNVISALAD---GN--KTH 282
QY 248 TEYKVALSLVDLAGSRATSTGACARLKEAGELIRSLTQRYVIAALADSSGKQKQ 307
Db 283 -TPYDSKSLTRITLQSLGGNATTVIVCCSPASFNSESTKSTLDGREATVKNVYVNE 341
QY 308 LVPTYDSVLTLKLDLGGNSKMTAIAISPADINFEETLSTLTADYSAKRINKHAYNE 367
Db 342 ELTAEEMKRYEKEKMARLAKVE 367
QY 368 D--PNAMIR-EL-KEELAOLAKLQ 389
RESULT 8
XX DE PCT-US94-04496-48 STANDARD; PRT; 1612 AA.
XX CC
XX AC xxxxxx
XX DE Sequence 48, Application US/08545860D
XX CC Sequence 48, Application US/08545860D
XX CC Patent No. 6040140
XX CC GENERAL INFORMATION:
XX DE Sequence 48, Application FC/TUS9404496
XX CC Sequence 48, Application FC/TUS9404496
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Croce, Carlo
XX CC APPLICANT: Canani, Eli
XX CC TITLE OF INVENTION: Diagnostic Therapeutics and Methods
XX CC TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
XX CC TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
XX CC NUMBER OF SEQUENCES: 86
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
XX CC ADDRESSEE: Norris
XX CC STREET: One Liberty Place, 46th floor
XX CC CITY: Philadelphia
XX CC STATE: Pennsylvania
XX CC COUNTRY: USA
XX CC ZIP: 19103
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US94/04496
XX CC FILING DATE:
XX CC CLASSIFICATION:
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: DeLuca Esq., Mark
XX CC REGISTRATION NUMBER: 33,229
XX CC REFERENCE/DOCKET NUMBER: TJU-1242
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: (215) 568-3100
XX CC TELEFAX: (215) 568-3439
XX CC INFORMATION FOR SEQ ID NO: 48:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 1612 amino acids
XX CC TYPE: amino acid
XX CC TOPOLOGY: linear
XX CC STRANDNESS: single
XX CC MOLECULE TYPE: protein
XX CC HYPOTHETICAL: NO
XX CC ANTI-SENSE: NO
XX CC SEQUENCE 1612 AA; 181981 MW; 13031792 CN;
Query Match 3.6%; Score 196; DB 4; Length 1612;
Best Local Similarity 34.5%; Pred. No. 2,01e-05;
Matches 38; Conservative 2; Mismatches 44; Indels 4; Gaps 4;
Db 383 LPYLVELSPGSDSRDKALRYLQLSVTEVTEKLDNLS-IQLFPGIOPHCDLTNNDC 441
QY 493 MPHVLNLSDDPLLA-E-CLWNLKPGQTRGVNAQQTQAEIRLNGSKILKEHCTFENVN 550
Db 442 VVTVPRSDAETVVEQRISETMLOGSKVKQVGASHVFKFVDPDSQDA 491
QY 551 VVTVPRSDAETVVEQRISETMLOGSKVKQVGASHVFKFVDPDSQDA 599
RESULT 9
XX DE US-08-545-860D-48 STANDARD; PRT; 1612 AA.
XX CC
XX AC xxxxxx
XX DE Sequence 48, Application US/08545860D
XX CC Sequence 48, Application US/08545860D
XX CC Patent No. 6040140
XX CC GENERAL INFORMATION:

APPLICANT: MEIKOIL, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37

SQ SEQUENCE 274 AA; 29378 MW; 452028 CN;
Query Match 1.8%; Score 98; DB 2; Length 274;
Best Local Similarity 41.3%; Pred. NO. 6.74e+01;
Matches 19; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
Db 141 SGGGGGGGGGGGAG-SAQVQLQSGPELVKPGASVKNCKA 185
| | | | | : | | | | : : : | : | : | |
Qy 390 SGGGGGGGGGGGPGVEESTPDPLEKQIVSIQQPDATVKMNSKA 435
Search completed: Mon Aug 21 15:42:50 2000
Job time : 19 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd
MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Aug 21 15:38:36 2000; MasPar time 22.31 Seconds
Tabular output not generated. 832.478 Million cell updates/sec

(TW)

Title: >US-09-235-416-1
Description: (1-784) from US09235416A.pep
Perfect Score: 5422
Sequence: 1 MSGGNIKVVYRFRNARE.....ELRQQQNMEEALKAKQDF 784
Scoring table: PAM 150
Gap 11
Searched: 188963 seqs, 23686106 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a:geneseq36
Statistics: Mean 37.958; Variance 188.559; scale 0.201
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	953	17.6	955	1	W03691	5,546-67
2	951	17.6	955	1	Leishmania chagasi K39	5,546-67
3	791	14.6	2954	1	K39 polypeptide of Lei	2,368-53
4	707	13.0	411	1	Amino acid sequence of	2,486-46
5	707	13.0	441	1	Drosophila kinesin N-t	2,486-46
6	707	13.0	975	1	Drosophila kinesin N-t	2,486-46
7	509	9.4	324	1	Drosophila kinesin	2,486-46
8	424	7.8	679	1	Leishmania antigen Lcg	5,836-30
9	211	3.9	1201	1	Human kinesin-related	4,748-23
10	196	3.6	1612	1	Drosophila sp. Cos2 pr	2,108-06
11	196	3.6	1612	1	Ras-binding protein pl	2,678-05
12	193	3.4	1829	1	Chimeric ALL-1/AP-6 pr	2,678-05
13	183	3.2	1354	1	Actin filament binding	2,358-04
14	183	3.2	1354	1	Renal cancer associate	2,128+00
15	183	3.2	1354	1	A modified rho target	2,128+00
16	113	2.1	350	1	Physiologically active	1,128+00
17	113	2.1	350	1	Amino acid sequence of	1,128+00
18	106	2.0	235	1	Human kinesin-related	1,448+01
19	108	2.0	320	1	41kD protein of T. coli	3,946+01
20	107	2.0	349	1	Mouse cysteine-rich se	2,966+01
21	108	2.0	350	1	Human cysteine-rich se	2,966+01
22	106	2.0	857	1	Staphylococcus aureus	2,966+01
23	109	2.0	1077	1	C3G protein.	2,566+01

ALIGNMENTS

RESULT 1

ID	W03691	standard; Protein; 955 AA.
AC	W03691:1997 (first entry)	
OS	OS-MAR-1997 (first entry)	
DE	Leishmania chagasi K39 antigen.	
KW	Leishmania chagasi; acidic ribosomal antigen; LCP0;	
KS	Leishmania chagasi; acidic ribosomal antigen; LCP0;	
QW	Leishmania chagasi.	
PN	W09633414-A2.	
PD	24-OCT-1996.	
PF	19-APR-1996; U05472.	
PR	21-APR-1995; US-428414.	
PA	(CORI-) CORIXA CORP.	
PI	Reed SG.	
DR	WPI: 96-485884/48.	
DR	N-PSDB: T42166.	
PT	New Leishmania acidic ribosomal P-protein family polypeptide - used to develop prods. for diagnosis, detection and protection against	
PT	Leishmania infections	
PS	Disclosure: Page 36-43; 76pp: English.	
CC	Compounds including polypeptides that contain at least an epitope of	
CC	the L. chagasi acidic ribosomal antigen LCP0 are useful in a variety	
CC	of immunoassays for detecting Leishmania infection. Portions of	
CC	LCP0 (T42166) contg. at least the 17 C-terminal amino acids (142165)	
CC	have been fused to a signal peptide to form an EMBL-tagged	
CC	protein that generated by the full length LCP0. A combinatorial	
CC	polypeptide may also be used, comprising an LCP0 epitope along with	
CC	an epitope derived from the Leishmania K39 antigen (T42166). pref.	
CC	the K39 repeat unit antigen having the sequence given in W03690.	
SC	Sequence 955 AA:	
Query Match 17.6%; Score 953; DB 1; Length 955;		
Best Local Similarity 43.5%; Pred. No. 5,546-67;		
Matches 177; Conservative 90; Mismatches 111; Indels 29; Gaps 18;		
DB	13	VKVSVRVRP.LNERENNAPEGKTVYAAKQAQVYVYKVGSSNGSAESMGTRRAVAD 72
QY	7	IKVVVVRVFNAREID-R-GAKTVYR-MEGNQTII-LTPPPGAEKARKSKR-TIMDGPKA 61
DB	73	QFDRVSVSVTPDCACTPAQVFRVYGLVQAFGNSCLPACFGTSCSKYPM 132
QY	62	PAFDRVSVFDR-KA-PNY-AREQDQDGLGVPLLDNFKSTNCIFRFGTSGRSYSM 118
DB	133	MGADVSAISGCEGNGVPRICLETAFKARSAVEAGCHSGVVELGYVYVNEVSDLLKPK 192
QY	119	MG-----Y-KGKGVIPRICDMFRINELQDNKLTCTVEVSYLETYNVRDLL-NP- 170

QY 339 ADINEETLSTLYADSAKRIKHNHVVNEDPNARMIRRELKEELAOLR 385

PN W05913061-AL.
 18-MAR-1999.
 PF 10-SEP-1998: U19231.
 PF 11-SEP-1997: US-058645.
 PR (REGC) UNIV CALIFORNIA.
 PI Cleveland DN, Goldstein LSI,
 DR WPI: 99-D29233/19.
 DR N-PSDB: X26819.
 DR N-PSDB: X26819.

Query Match	14.6%	Score	791;	DB 1;	Length	2954;
Best Local Similarity	39.9%	Pred. No.	2.36e-53;			
Matches	132;	Conservative	92;	Mismatches	90;	Indels 17; Gaps 13;
Db	43	KSF-NDFRWFNSHSTQIYQIQAIVPIIRSLALQYNGCTTFAYGQSGKTTMMGTTPNSL	101			
Qy	66	RSTFSDNAPNARQEDLQDQGVLPDLPAGFNCIFAYGQSGKSFSMMGATGEH	125			
Db	102	GIIPQATQEVFKIQTIEP-NREFL-LRVSYWEIYNETVKOLLCDDRKKPLEIRDPNR	158			
Qy	126	GVPIRCQDFRINLEQKANKLCTVYSYELIENRVOLL-NSTYKGNLAVREHST	184			
Db	159	NYVYADITELVYVPHVITQIKKGNKHVGETKNDSSRSHFTFMATVESDRNDPT	218			
Qy	185	GPYVEDLKLAVRSQEIENLMDGSENKARTVAATNNVSSRSRHFVLTLT-TQKHDE-	242			
Db	219	NSENCQGNVYSHLNLVDLAGSERASQTGAGVELKEGCNTNRESLTGOVKKLED--	275			
Qy	243	ETKM-DTE-KVAKISLYDLASERASTGNGARLEKGEINRSLSLTGRVIAALADSS	300			
Db	276	G-QA-GGFNTVEDSKLTRILQNSIGNATVICTITP--VSPDETSLTQFQSTAKVHR	331			
Qy	301	GKQKKNQLPYDSEVLTLLADSLGNSWTAMIAALSPADINFEETLSTLRVYDASAKIK	360			
Db	332	NTPHVNVEDLDEALKHYKBEITDOLKKOLEN	362			
Qy	361	HNAYVND-PNABWIRELKEALQALSKLOS	390			

ID W2745 standard; protein; 411 AA.
 AC W2745;
 DT 11-JAN-1999 (first entry)
 DE Drosophila kinesin N-terminal 411 amino acid residues.
 DT Drosophila kinesin N-terminal 411 amino acid residues.
 DE Drosophila kinesin N-terminal 411 amino acid residues.
 KW complex mixture; motor protein; separation; hybridisation; target site;
 KW complex mixture; motor protein; separation; hybridisation; target site;
 KW complex mixture; motor protein; separation; hybridisation; target site;
 KW complex mixture; motor protein; separation; hybridisation; target site;
 OS Drosophila sp.
 PN US980659-A.
 PP 03-NOV-1998. 713815
 PR 13-SEP-1996; US-713815
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Stewart RJ;
 DT WPI: 98-609236/51.
 DR Separation of selected molecules, e.g. DNA, from complex mixtures -
 PT uses specific apparatus to allow the selected molecule to bind to
 PT motor proteins, and be actively transported and separated away along
 PT micro:tubules
 PS Claim 3; Column 25-28; 24pp; English.
 CC A method has been developed of separating a selected molecule from a
 CC mixture of molecules. The method comprises: (a) a separation device
 CC comprising a loading reservoir and a receiving reservoir coupled by a
 CC channel with microtubules immobilised on its surface and aligned parallel
 CC to a longitudinal axis of the channel; (b) loading the loading reservoir
 CC with an aqueous solution of the mixture of molecules; (c) adding a motor-
 CC ligand composition and ATP to the solution, where the motor-ligand
 CC comprises, (1) a processive motor capable of attaching to the immobilised
 CC microtubules, and moving in the presence of ATP as source of chemical
 CC energy, and (2) a ligand coupled to the motor protein, where the ligand
 CC is capable of binding to the selected molecule, so that the ligand binds the
 CC selected molecule and the motor protein attaches to the immobilised
 CC microtubules and transports the bound selected molecules along the
 CC receiving reservoir; and (d) removing the selected molecules from the
 CC separation of specific molecules from complex mixtures. The molecule to
 CC be separated (e.g. DNA) binds to the motor protein due to the presence of
 CC the specific binding ligands. Activation of these enables them to travel
 CC down a preformed channel in a specially made piece of apparatus. They can
 CC then be removed easily without contaminants of other mixture particles.
 CC The present sequence represents the N-terminal 411 amino acid residues of
 CC Drosophila kinesin for use in the method of the invention.
 SQ Sequence 411 AA;

Query Match 13.0%; Score 707; DB 1; Length 411;
 Best Local Similarity 42.3%; Pred No. 2,486-46;
 Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;
 Db 55 FDKVFKPNASQKVEYNEAKSIYTDVLAGYNGTIFAYGOTSSGKTHMEGVGDSYKQGI 114
 QY 71 FDKNAPYARQEDLPQDLGVPLLDNAFKYNNCFAYGOTGSGKSYNMG-YGKE--HGV 127
 Db 115 IPRIVNDIFNHYAM--EVLNDEPHIKVSYEYIMOKIRDLDDVS-KVNLVSHEDKNRVY 171
 QY 128 IPRICQDMFRINELQDKNLCTCTVFSYLEIYNERVRLDLPSTGKGLKVRHPSTGYP 187
 Db 172 VKGATERFVSPEDVFVEIEGKSNRIHATVNMNEHSRSHSVFLNKVQENLEOKKL- 230
 QY 188 VEDLAKLVRSFOEINLMDEGNKARTVAATNMNETSSRSHAVFTLTQKHDEETKMD 247
 Db 231 S---GKLYLVLDAGSEKSVKTAGETVLDKANKNSLSALGNVISALAD---GN--KTH 282
 QY 248 TEKRAKILSLVDLAGSERATSGATGARKGAEINRSLTGLRVIALADMSGKKQKMD 307
 Db 283 -IPIRDSKRLTLOESLGNARTYIYCSPASNESETKSTLDFGRAKTVKYNVCVNE 341
 QY 308 LVPYEDSVLTWLLADSLGNSMTANIALISPADINFEETLSTLYADSKRIKHAVYNE 367
 Db 342 ELTAEEKRVRVEKEKEKNAKLGKVE 367
 QY 368 D--PNARMIR-EL-KEELAQLRSKLQ 389

RESULT 5
 ID W2744 standard; protein; 441 AA.
 AC W2744;
 DT 11-JAN-1999 (first entry)
 DE Drosophila kinesin N-terminal 441 amino acid residues.
 DT Drosophila kinesin N-terminal 441 amino acid residues.
 KW complex mixture; motor protein; separation; hybridisation; target site;
 KW complex mixture; motor protein; separation; hybridisation; target site;
 KW complex mixture; motor protein; separation; hybridisation; target site;
 OS Drosophila sp.
 PN US980659-A.
 PP 03-NOV-1998. 713815
 PR 13-SEP-1996; US-713815
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Stewart RJ;
 DT WPI: 98-609236/51.
 DR Separation of selected molecules, e.g. DNA, from complex mixtures -
 PT uses specific apparatus to allow the selected molecule to bind to
 PT motor proteins, and be actively transported and separated away along
 PT micro:tubules
 PS Claim 3; Column 23-26; 24pp; English.
 CC A method has been developed of separating a selected molecule from a
 CC mixture of molecules. The method comprises: (a) a separation device
 CC comprising a loading reservoir and a receiving reservoir coupled by a
 CC channel with microtubules immobilised on its surface and aligned parallel
 CC to a longitudinal axis of the channel; (b) loading the loading reservoir
 CC with an aqueous solution of the mixture of molecules; (c) adding a motor-
 CC ligand composition and ATP to the solution, where the motor-ligand
 CC comprises, (1) a processive motor capable of attaching to the immobilised
 CC microtubules, and moving in the presence of ATP as source of chemical
 CC energy, and (2) a ligand coupled to the motor protein, where the ligand
 CC is capable of binding to the selected molecule, so that the ligand binds the
 CC selected molecule and the motor protein attaches to the immobilised
 CC microtubules and transports the bound selected molecules along the
 CC receiving reservoir; and (d) removing the selected molecules from the
 CC separation of specific molecules from complex mixtures. The molecule to
 CC be separated (e.g. DNA) binds to the motor protein due to the presence of
 CC the specific binding ligands. Activation of these enables them to travel
 CC down a preformed channel in a specially made piece of apparatus. They can
 CC then be removed easily without contaminants of other mixture particles.
 CC The present sequence represents the N-terminal 441 amino acid residues of
 CC Drosophila kinesin for use in the method of the invention.
 SQ Sequence 441 AA;

Query Match 13.0%; Score 707; DB 1; Length 441;
 Best Local Similarity 42.3%; Pred No. 2,486-46;
 Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;
 Db 55 FDKVFKPNASQKVEYNEAKSIYTDVLAGYNGTIFAYGOTSSGKTHMEGVGDSYKQGI 114
 QY 71 FDKNAPYARQEDLPQDLGVPLLDNAFKYNNCFAYGOTGSGKSYNMG-YGKE--HGV 127
 Db 115 IPRIVNDIFNHYAM--EVLNDEPHIKVSYEYIMOKIRDLDDVS-KVNLVSHEDKNRVY 171
 QY 128 IPRICQDMFRINELQDKNLCTCTVFSYLEIYNERVRLDLPSTGKGLKVRHPSTGYP 187
 Db 172 VKGATERFVSPEDVFVEIEGKSNRIHATVNMNEHSRSHSVFLNKVQENLEOKKL- 230
 QY 188 VEDLAKLVRSFOEINLMDEGNKARTVAATNMNETSSRSHAVFTLTQKHDEETKMD 247
 Db 231 S---GKLYLVLDAGSEKSVKTAGETVLDKANKNSLSALGNVISALAD---GN--KTH 282
 QY 248 TEKRAKILSLVDLAGSERATSGATGARKGAEINRSLTGLRVIALADMSGKKQKMD 307
 Db 283 -IPIRDSKRLTLOESLGNARTYIYCSPASNESETKSTLDFGRAKTVKYNVCVNE 341
 QY 308 LVPYEDSVLTWLLADSLGNSMTANIALISPADINFEETLSTLYADSKRIKHAVYNE 367
 Db 342 ELTAEEKRVRVEKEKEKNAKLGKVE 367
 QY 368 D--PNARMIR-EL-KEELAQLRSKLQ 389

RESULT 6

ID W72746 standard; Protein: 975 AA.

AC W72746 AC

DT 11-JAN-1999 (first entry)

OS Drosophila kinesin.

KW Drosophila kinesin;

KW complex mixture; motor protein; separation; hybridisation; target site;

KW microtubule.

OS Drosophila sp. Location/Qualifiers

FT Key Misc_difference 557 /note= "encoded by AAT"

FT PN US5830659-A.

PD 03-NOV-1998.

PP 13-SEP-1996: 713815.

PR 13-SEP-1996: US-713815.

PA (UTAH) UNIV UTAH RES FOUND.

ST Stewart RJ.

TI WPI: 98-609236/51.

DR N-PSDB: V67162.

PPT Separation of selected molecules, e.g. DNA, from complex mixtures -

PPT uses specific apparatus to allow the selected molecule to bind to

PPT motor proteins, and be actively transported and separated away along

PPT microtubules

PPT Disclosure: Column 17-24: 24pp: English.

PPT A method has been developed of separating a selected molecule from a

PPT mixture of molecules. The method comprises: (a) a separation device

PPT comprising a loading reservoir and a receiving reservoir coupled by a

PPT channel with microtubles immobilised on its surface and aligned parallel

PPT to a longitudinal axis of the channel; (b) loading the loading reservoir

PPT with an aqueous solution of the mixture of molecules; (c) adding a motor-

PPT ligand composition and ATP to the solution, where the motor-ligand

PPT comprises, (i) a processing motor capable of attaching to the immobilised

PPT microtubules, and moving in the presence of ATP as source of chemical

PPT energy, and (ii) a ligand coupled to the motor protein, where the ligand

PPT is capable of binding the selected molecule, so that the ligand binds the

PPT selected molecule and the motor protein attaches to the immobilised

PPT microtubules and transports the bound selected molecules along the

PPT receiving reservoir; and (d) removing the selected molecule from the

PPT separation of specific molecules from complex mixtures. The molecule to

PPT be separated (e.g. DNA) binds to the motor protein due to the presence of

PPT the specific binding ligands. Activation of these enables them to travel

PPT down a preformed channel in a specially made piece of apparatus. They can

PPT then be removed easily without contaminants of other mixture particles.

PPT The present sequence represents Drosophila kinesin from the present

PPT invention. 975 AA:

SO

Query Match	13.0%	Score 707;	DB 1;	Length 975;
Best Local Similarity	42.38;	Prod No. 2,48e-46;		
Matches 138;	Conservative 77;	Mismatches 91;	Indels 20;	Gaps 12;
55	FDKVFKNASQEKVYNEAAKSI	IVTDVLAGVYKTFIFAYGQTSFGSKTHMECVIGSVKQIG	114	
71	FDKNAPNARQEDFLDQGLVFLD	NAFNGVNCIFAYGQTSKSYKMG	-HGV	127
115	IPRVINDIFNHIYAM--EVNLEPH	KVSYVEYIMDKIRDLLOVS--KYNLSVHEOKNRPVP	171	
128	IPRICODMFRINELQKQKNI	LTCTVEYSLEYINERVLDLLNPSTGNLKVREHPSTGYP	187	
172	VKGATRVFSSPEDVFEVIEEGKS	NRHIAVTNNHNSRSHSVFLINVKQENLQKKU-	230	
186	VEDLAKLVRFQFQELNMEGKAT	VDPAKTNKSLGALVYISALAD--GN-KTH	282	
231	S--GKLVYDGLAGEKVTGAGCTV	LDPAKTNKSLGALVYISALAD--GN-KTH	282	
248	TEKVAKISLVLDAGSERATSTGAT	CARLKGAEINRSLTGLRVIALADMSQCKQKQK	307	
283	-IPYRDSKLTIRIQESLGNARTIV	ICCPASFNSESTKSTLDFGRRAKTVKVNVCY	341	
308	LVYPRDSVLTWLLKSLGAGSM	FTAMIAISPADIINFETLSLTVADSAKRILKHAHVNE	367	

342 DB ELTAENKRYEKEKRNARKLGKVE 367
 368 QY D--FNARMIR-EL-KEELAQRSLKQ 389

RESULT 7
 ID W70235 standard; Protein; 324 AA.
 AC W70235;
 13-NOV-1998 (first entry)
 DE Leishmania antigen LcgSP10 protein.
 KW Leishmania antigen; immune response; infection detection; therapy;
 DE humoral response induction; cellular response induction; cancer;
 KW interleukin-12 production.
 OS Leishmania chagasi.
 OS Leishmania chagasi.
 Key Location/Qualifiers
 FT Misc_difference 79
 FT Misc_difference 96 /note= "unspecified amino acid"
 FT Misc_difference 96 /note= "unspecified amino acid"
 FT W0983045-A2.
 PN 13-AUG-1998.
 PF 12-FEB-1998; U03002.
 PF 27-AUG-1997; U0302609.
 PF 12-FEB-1997; U0302609.
 PF 12-FEB-1997; U0302609.
 PF (CORL-) CORIXA CORP.
 PF (Campos-Neto A, Dillon DC, Reed SG, Skeiky YA, Webb JR;
 WPI. 96-447242/38.
 DR NPDB: W47580.
 DR New immunogenic fragments of Leishmania antigens and related nucleic
 acid, vectors and host cells - are useful for diagnosis, prevention
 and treatment of leishmaniasis, also to induce production of
 interleukin-12 generally
 PT Claim 13; Page 128-129; 194pp; English.
 PT This sequence encodes a Leishmania antigen (Lag) of the invention,
 designated LcgSP10. Compositions and vaccines containing the protein are
 used to generate a protective or therapeutic immune response against the
 Leishmania species donovani, chagasi, infantum, major, amazonensis,
 braziliensis, panamensis, tropica or guyanensis. They can also be used
 to detect infection (in a skin test). The compositions induce a humoral
 and/or cellular response, specifically of Th1 type, particularly
 including induction of interleukin-12 (IL-12) production. They may thus
 be used more generally to treat any condition (e.g. bacterial, viral or
 protozoal infection, or cancer) which responds to IL-12.
 CC Query 324 AA;

Sequence Match 9.4%; Score 509; DB 1; Length 324;
 Best Local Similarity 42.2%; Pred. No. 5.83e-30;
 Matches 76; Conservative 47; Mismatches 53; Indels 4; Gaps 4;

145 DB GGIIIPACTDLEGLRANKDSFTVEYSYIYNEKVFLLRPNVDLIRNSPN 204
 125 QY HVVPIRQCDMFRNEIQ-KDMLTCIVSVYELIYNERVOLLNFTKGNLREHPS 183
 205 SCPIELTTHWWSKE-EDVAVIRKGMOERHEDVQVKNHSITVLGVDRDLADLSONK 263
 184 QY GVPIVEDIA-KLVRSFQETENLMDGKATGKATVARNKESRSHALFNIVOLSMD 242
 264 SDN-AFOMSKNLVDLASSGFRGAGNPHEDVQVKNHSITVLGVDRDLADLSONK 322
 243 QY ETKMDYEVKAVISVDLASSGFRATSGTGARKLKEAGINRSLTGLRVIALADMSSGK 302

RESULT 8
 ID W88456 standard; Protein; 679 AA.
 AC W88456;
 10-MAY-1999 (first entry)
 DE Human kinesin-related protein KINRPLP.
 KW Kinesin-related protein; KINRPLP; human; cancer; apoptosis;
 DE cell proliferation; inflammation; therapy; diagnosis; ss.
 OS Homo sapiens.
 OS Homo sapiens.
 Key Location/Qualifiers
 FT Binding site 286...293

FT FT Domain
FT FT /note= "ATP-binding P-loop"
FT FT 424. .435
FT FT /note= "kinesin motor domain signature"
FT FT 9. .11
FT FT /note= "Asn is N-glycosylated"
FT FT 106. .109
FT FT /note= "Asn is N-glycosylated"
FT FT 244. .247
FT FT /note= "Asn is N-glycosylated"
FT FT 406. .459
FT FT /note= "Asn is N-glycosylated"
FT FT 127. .130
FT FT /note= "potential cAMP- and cAMP-dependent protein
FT FT kinase phosphorylation site"
FT FT 208. .211
FT FT /note= "potential cAMP- and cAMP-dependent protein
FT FT kinase phosphorylation site"
FT FT 4. .7
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 27. .30
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 108. .111
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 187. .199
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 273. .280
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 338. .341
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 427. .430
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 441. .444
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 447. .450
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 582. .589
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 634. .637
FT FT /note= "potential casein kinase II phosphorylation
FT FT site"
FT FT 233. .241
FT FT /note= "potential tyrosine kinase phosphorylation
FT FT site"
FT FT 329. .336
FT FT /note= "potential tyrosine kinase phosphorylation
FT FT site"
FT FT 58. .60
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT 73. .75
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT 88. .90
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT 126. .128
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT 246. .248
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT 266. .268
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"

FT FT Modified_site 290. .292
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 301. .303
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 344. .346
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 392. .394
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 405. .407
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 516. .518
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 608. .610
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT Modified_site 656. .658
FT FT /note= "potential protein kinase C phosphorylation
FT FT site"
FT FT X0985064-A1.
FT FT 79-108-1998.
FT FT 19-JUN-1998; UI28556
FT FT 19-JUN-1997; US-878865
FT FT (INCY-) INCYTE PHARM INC.
FT FT Au-Young J. Lal P. Shah P;
FT FT WPI: 99-080955/07.
FT FT N-PSDB: X06945.
FT FT New kinesin-related protein - useful for treating cancer and
FT FT inflammation
FT FT Claim 1: Page 49-50; 72pp; English.
FT FT This is the amino acid sequence of human kinesin-related protein
FT FT (KINRPL), as deduced from a consensus cDNA sequence (see X06945).
FT FT KINRPL shares 97% identity with murine kinesin-related protein
FT FT XIP2. The invention provides expression vectors, host cells,
FT FT agonists, antibodies and antagonists, as well as methods for
FT FT treating disorders associated with expression of KINRPL. KINRPL
FT FT and its agonists are used to stimulate cell proliferation, and to
FT FT treat a disorder associated with increased apoptosis. Antagonists
FT FT of KINRPL or its fragments may be used to treat cancer, particularly,
FT FT other infectious or genetic immunodeficiencies, neurodegenerative
FT FT diseases such as Alzheimer's disease, Parkinson's disease,
FT FT cerebellar degeneration; myelodysplastic syndromes such as aplastic
FT FT anemia; ischemic diseases such as myocardial infarction, stroke
FT FT and reperfusion injury; toxin-induced diseases such as
FT FT alcohol-induced liver disease, cirrhosis and lathyrism; wasting
FT FT diseases such as cachexia and osteoporosis; viral infections with
FT FT as causes caused by hepatitis B and C; and diseases associated with
FT FT inflammation including adult respiratory distress syndrome,
FT FT allergy, asthma, arteriosclerosis, bronchitis, emphysema,
FT FT hyperosinophilia, myocardial or pericardial inflammation,
FT FT rheumatoid arthritis, Addison's disease, AIDS, anaemia,
FT FT dermatitis, dematomyositis, diabetes mellitus, glomerulonephritis,
FT FT multiple myeloma, osteoarthritis, osteoporosis, psoriasis,
FT FT polycystic kidney disease, polymyositis, scleroderma, Sjogren's
FT FT syndrome, autoimmune thyroiditis, complications of cancer,
FT FT extracorporeal circulation, viral, bacterial, fungal, parasitic,
FT FT protozoal and helminthic infections and trauma.
FT FT Sequence 679 AA;

Query Match 7.8%; Score 424; DB 1; Length 679;
Best Local Similarity 35.7%; Pred. No. 4,74e-23;
Matches 133; Conservative 80; Mismatches 121; Indels 39; Gaps 23;

RESULT	11
ID	R66457 standard; Protein; 1612 AA.
AC	R66457:

RESULT 13
 ID Y07082 standard; Protein; 1354 AA.
 AC 02-JUL-1999 (first entry)
 DE Renal cancer associated antigen precursor sequence.
 DT Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.
 OS Homo sapiens.
 PN W09904265-A2.
 PD 28-JAN-1999.
 PF 15-JUL-1998: U14679.
 PR 22-JUN-1998: US-102322.
 PR 17-JUL-1997: US-886164.
 PR 10-OCT-1997: US-061599.
 PR 10-OCT-1997: US-061765.
 PR 10-OCT-1997: US-948705.
 PR 11-OCT-1997: GB-021697.
 PA (LUDW.) LUDWIG INST CANCER RES.
 PI Chen Y, Gout I, Gure A, Ohare M, Obata Y, Old LJ,
 PI Pfrendschuh M, Sahin U, Scanlan MJ, Stockert E.
 PI Tureci O.
 DR WPI; 99-132448/11.
 DR New isolated cancer associated nucleic acids and polypeptides -
 PT isolated using sera from cancer patients, used to develop products
 PT for the diagnosis, monitoring or treatment of cancers
 PS disclosure; Page 491-494; 787pp; English.
 CC The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an HLA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer. 1354 AA.
 SQ Sequence

Query Match 2.28; Score 120; DB 1; Length 1354;
 Best Local Similarity 28.1%; Pred. No. 5.12e+00;
 Matches 41; Conservative 32; Mismatches 66; Indels 7; Gaps 6;
 Db 849 FOYFSTL-YKTQVKELKEEIEENRNKKIQLONEKETLATQDLAETKAESEQLARG 907
 QY 344 EETLSTLYADSAKRKKHVVNEDPNARMIRELELAQLRSKLSQSGGGGGGSGG 403
 Db 908 LLEQFVELTQESKKAASRNQBITDKDHTVSRLEFANSMLTKDTILRRE-NEELTEKM 966
 QY 404 PVESYPPDTPLEKQIVSIQPDATVK--KMSKAEIVEQ-LNQS-EKLYRDLNQTWEKL 459
 Db 967 KKAEEYKLEKEEIEISNLKAAFEKNI 992
 QY 460 AKTEEIHK-EREAALEELGISIEKGF 484

RESULT 14
 ID W71020 standard; Protein; 1354 AA.
 AC 27-OCT-1998 (first entry)
 DE A modified Rho target protein kinase p160 protein.
 KW protein kinase activity; Rho protein; preparation;
 KW therapeutic composition.
 OS Homo sapiens.
 PN J10191985-A.
 PD 28-JUL-1998.
 PF 17-JAN-1997: 019870.

PR 17-JAN-1997: JP-019870.
 PA (KIRI.) KIRIN BREWERY KK.
 DR WPI; 98-460110/40.
 DR N-PSDB; V42941.
 PT New protein exhibiting protein kinase activity - is not capable of
 PT binding to active Rho protein or its derivative, used, e.g.
 PT therapeutically.
 PS Claim 1: Fig 1; 60pp; Japanese
 CC The present sequence encodes a protein which exhibits protein kinase
 CC activity and is not capable of binding to active Rho protein or its
 CC derivative. The materials may be used for the preparation of
 CC therapeutic compositions.
 SQ Sequence 1354 AA.

Query Match 2.28; Score 120; DB 1; Length 1354;
 Best Local Similarity 28.1%; Pred. No. 5.12e+00;
 Matches 41; Conservative 32; Mismatches 66; Indels 7; Gaps 6;
 Db 849 FOYFSTL-YKTQVKELKEEIEENRNKKIQLONEKETLATQDLAETKAESEQLARG 907
 QY 344 EETLSTLYADSAKRKKHVVNEDPNARMIRELELAQLRSKLSQSGGGGGGSGG 403
 Db 908 LLEQFVELTQESKKAASRNQBITDKDHTVSRLEFANSMLTKDTILRRE-NEELTEKM 966
 QY 404 PVESYPPDTPLEKQIVSIQPDATVK--KMSKAEIVEQ-LNQS-EKLYRDLNQTWEKL 459
 Db 967 KKAEEYKLEKEEIEISNLKAAFEKNI 992
 QY 460 AKTEEIHK-EREAALEELGISIEKGF 484

RESULT 15
 ID W23654 standard; Protein; 1354 AA.
 AC W23654;
 DT 13-OCT-1997 (first entry)
 DE Physiologically active protein p160.
 KW Rho binding activity; protein kinase; protein binding; host cell;
 KW recombinant production; human.
 OS Homo sapiens.
 PN J09135683-A.
 PD 27-MAY-1997.
 PF 25-JUN-1996: 184102.
 PF 14-SEP-1995: JP-262553.
 PA (KIRI.) KIRIN BREWERY KK.
 DR WPI; 97-33590/31.
 DR N-PSDB; T78203.
 PT Physiologically active protein p160 - has rho binding activity and
 PT protein kinase activity
 PS Claim 6; Page 21-24; 53pp; Japanese.
 CC The present sequence represents the physiologically active protein
 CC p160, which has active Rho protein-binding and protein kinase
 CC activities. The nucleotide sequence can be put into a vector which can
 CC then be used to transform a host cell. The host cell can be cultured
 CC for the recombinant production of the p160 protein. The p160 protein
 CC can be used in a method to screen for compounds that inhibit the
 CC protein kinase activity.
 SQ Sequence 1354 AA.

Query Match 2.28; Score 120; DB 1; Length 1354;
 Best Local Similarity 28.1%; Pred. No. 5.12e+00;
 Matches 41; Conservative 32; Mismatches 66; Indels 7; Gaps 6;
 Db 849 FOYFSTL-YKTQVKELKEEIEENRNKKIQLONEKETLATQDLAETKAESEQLARG 907
 QY 344 EETLSTLYADSAKRKKHVVNEDPNARMIRELELAQLRSKLSQSGGGGGGSGG 403
 Db 908 LLEQFVELTQESKKAASRNQBITDKDHTVSRLEFANSMLTKDTILRRE-NEELTEKM 966
 QY 404 PVESYPPDTPLEKQIVSIQPDATVK--KMSKAEIVEQ-LNQS-EKLYRDLNQTWEKL 459
 Db 967 KKAEEYKLEKEEIEISNLKAAFEKNI 992
 QY 460 AKTEEIHK-EREAALEELGISIEKGF 484

Mon Aug 21 15:58:33 2000

US-09-235-416-1.rag

Page 9

Search completed: Mon Aug 21 15:39:03 2000
Job time : 27 secs.

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 M0506LH

 (TM)

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MPsrchLpp protein - protein database search, using Smith-Waterman algorithm
 Run On: Mon Aug 21 15:39:19 2000; MagPar time 40.22 Seconds
 919,448 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-235-416-1
 Description: (1-784) from US092354156A.pap
 Perfect Score: 5422
 Sequence: 1 MSGGGNIKVVVRVRRPNARE.....ELRQQQAEALTKAQEF 784

Scoring table:
 PAM 150
 Gap 11

Searched: 142080 seqs, 47172406 residues
 Post-processing: Minimum Match 0%

Listing first 45 summaries
 Database: p1r64

Statistics: Mean 53.618; Variance 119.927; scale 0.447
 1p1r1 2p1r2 3p1r3 4p1r4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result	Query	Match	Length	Pred. No.
No.	Score		ID	Description
1	2217	40.1	1150	kinesin-like protein
2	2176	40.1	A55289	kinesin family protein
3	1975	36.4	1 JN0114	kinesin-related prote
4	1501	36.4	T15822	kinesin-like protein
5	1391	33.8	2 T16759	kinesin-73 fruit fl
6	1291	33.8	1938	hypothetical protein
7	1008	18.6	699	kinesin-related prote
8	962	17.7	701	kinesin-related prote
9	962	17.7	742	kinesin-related prote
10	953	17.6	955	LcKin kinesin-related
11	942	17.4	747	kinesin-related prote
12	900	16.6	284	kinesin-related prote
13	897	16.5	A55236	kinesin-related prote
14	870	16.0	786	kinesin homolog KHP1
15	857	15.8	A53939	kinesin-like protein
16	850	15.7	1121	kinesin-related prote
17	846	15.6	1231	microtubule-associate
18	833	15.5	623	kinesin osa-3 - Caeno
19	825	15.2	1252	chromokinesin - chick
20	825	15.2	1256	kinesin-like protein
21	793	12.7	2653	kinesin heavy chain -
22	793	12.7	2653	centromere protein 2
23	791	14.6	2994	kinesin-related prote

ALIGNMENTS

```

RESULT 1
ENTRY A55289 #type complete
TITLE kinesin-like protein KIF1B - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
ACCESSIONS A55289
REFERENCE A55289
#authors Nangaku, M.; Sato-Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura, R.; Yamazaki, H.; Hirokawa, N.
#journal Cell (1994), 79:1209-1220
#title KIF1B, a novel microtubule plus end-directed monomeric motor protein that mediates transport of mitochondria.
#cross-references PMID:95094236
#accession A55289
#status preliminary
#molecule_type mRNA
#residues 1-1150 #label NAN
#cross-references GB:017577; NID:9407338; PIDN:BA04503.1; PID:d1005029; PID:g407339
CLASSIFICATION #superfamily kinesin-related protein KIF1B; kinesin motor domain homology
KEYWORDS P-loop
FEATURES
6-354 #domain kinesin motor domain homology #label KMOT\
97-104 #region nucleotide-binding motif A (P-loop)
SUMMARY #length 1150 #molecular-weight 130278 #checksum 5200
Query Match 40.9%; Score 2217; DB 1; Length 1150;
Best Local Similarity 35.3%; Red. No. 0.00e+00;
Matches 340; Conservative 132; Mismatches 114; Indels 29; Gaps 20;
Db 1 MSGAS-VKVVAVRVPFNSRFSKESKCTIOMOGNSTIINP-----K--NP-K---EAPK 48
Qy 1 MSGGGNIKVVVRVRRPNARELDRGAKCIVRMESGNOTILTPPGAEKARKSKCTIMDGP 60
Db 49 SFSDYSYWSHSPEDFCAQRNVYNDIGKMLLHAFEGYNYVCIFYAGTGAGKSYPM 108
Qy 61 AFAPFDSYWSFDK-NAPNVAQEDLFQDLGVLDFNAFKGYNVCIFYAGTGAGKSYPM 119
Db 109 GQESQAVITPOLCEELFEKIND-NCNEDSYSEVSYMEYTCYERVOLLNPKNGKL 167
Qy 120 GYGKE-HGVT-PRICOMDFRINELODKMLTCVSEYLETINERVOLLNPKNGKL 177
Db 168 VREHPLLGPVDELSKLVSYDFTADLADAGNKAQVTAARVANNETSSRSHVFTVPTQ 227
Qy 178 VREHPSTGFVDELDKLVRSFQENLADGKNKAQVTAARVANNETSSRSHVFTVPTQ 237

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Db 228 KKQDPETNLSTKRSKISLVDLGSRADSTGAKGTRKKEGANINKSLTLGKVISALAE 287
Qy 238 KWIIDEETKMTKRVAKISLVDLGSRADSTGATGARLKEGAENRSLSTLGRVIAALAD 297
Db 288 VSK-KKKKTDFTPIYRDSVLTWLLRNLGNSTAMVAALSPADINDETSLTRYADRAK 346
Qy 298 MSSGKKKNOLPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETSLTRYADSAK 357
Db 347 QIKCANVINEDPNNAKLVRELKBEVTRKDLRAQGLGDI- IDTSMGSLTSS-PSSCSLNS 404
Qy 358 RIKNHAVYVNDPNNAIRLRELKBEVTRKDLRAQGLGDI- IDTSMGSLTSS-PSSCSLNS 417
Db 405 QVGLSVTSIQRIINPTGGEBAIRLKESEKRTIAELNETWEEKLRKTEARTEAREALLA 464
Qy 418 QI-V-SIQPDATVKKMSKAE-IVQNLQSEKLYRDUNQWTEELKATEEIIHKEAREALE 474
Db 465 EMGVAIRERDGDIGVFPKPKTHLVNLNEDPLMSECLLYIKDGITRVGQADAEERDVI 524
Qy 475 ELGISI-E-KGFGVGYHSKEMPHVNLNEDPLMSECLLYIKDGITRVGQADAEERDVI 532
Db 525 LSGAIHKEEHLFRSEKNTGVEVITLPEKSEYTYNGKRVKVPQVLRNSRITNGKXH 584
Qy 533 LNSGKILKEHCTF-E--VNDNV-VTVPNKAAVWVNGVRIDKPTRLSRGYRIILGDFH 587
Db 585 VFRNHPQARARE 599
Qy 588 IFRNHPQARAREQ 602

RESULT 2 A56921 #type complete
ENTRY Kinesin family protein Kiria - mouse
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 13-Aug-1999
ACCESSIONS A56921
REFERENCE Okada, Y.; Yamazaki, H.; Sekine-Aizawa, Y.; Hirokawa, N.
#authors Cell (1995) 81:769-780
#journal The neuron-specific kinesin superfamily protein KIFIA is a
#title unique monomeric motor for anterograde axonal transport of
synaptic vesicle precursors.
#cross-references MIM:352324
#accession A56921; translated from GB/EMBL/DBJ
#molecule_type RNA
#residues 1-1695 #label RES
#cross-references GB:D29951; NID:976234; PID:9976235
CLASSIFICATION #superfamily kinesin-related protein unc-104; kinesin motor
domain homology; plectatrin repeat homology
KEYWORDS P-loop
FEATURE 6-360
#domain kinesin motor domain homology; #label KMT0\
#region nucleotide-binding motif A (P-loop)
#length 1695 #molecular-weight 191773 #checksum 7412
SUMMARY
Query Match 40.1%; Score 2176; DB 2; Length 1695;
Best Local Similarity 54.0%; Pred. No. 0.00e+00;
Matches 334; Conservative 133; Mismatches 121; Indels 31; Gaps 19;

Db 1 MAGAS-VKAVVRPFNSRMSRSDSKCIOMSGSTTVNPE-----K-Q-P-K--ETPK 48
Qy 1 MSSGGNIKVVRPNAREIDRGACIVRMENQOTILPPPGAEKAKSGKGTMDGPK 60

Db 49 SFSFDYSWHTSPEDINVASOKVYRDIGEMLOHAFEGYVNCIFAYGTGAGKSYTM 108
Qy 61 AFARFYSWFKD-NAPNARQEDLFQDLGVPLDNLNAPKYNNCIFAYGTGAGKSYTM 119

Db 109 GKQKDOGGIIPOLCEDLSRINDTND-NMYSVSEVSYMEIYCEVRDLNPNKGNLR 167
Qy 120 G-YGKEH-GVPIRICQDMFRINELQDKNLCTVYSVLRYNERNVRDLNPNSTGNLK 177

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Db 166 VREHPUGIYPTVEDLSKLVATSYNDIQLMDSGNKPRVTAATNMNETSSSHAVENIIFTQ 227
Qy 178 VREHPSTGYVEDLAKLVRSFORLENIDECNKARTVTAATNMNETSSSHAVFTLTQ 237
Db 228 KRIDAETNITTEKRSKISLVDLGSRADSTGAKGTRKKEGANINKSLTLGKVISALAE 287
Qy 238 KWIIDEETKMTKRVAKISLVDLGSRADSTGATGARLKEGAENRSLSTLGRVIAALAD 297
Db 288 MDSGNPKKKKKTDFTPIYRDSVLTWLLRNLGNSTAMVAALSPADINDETSLTRY 347
Qy 298 MSSG-----KOKKN-OLVYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETSLTRY 352
Db 348 ADRAKQIRCANINEDPNNAKLVRELKBEVTRKDLRAQGLGDI- IDTSMGSLTSS-PSSCSLNS 406
Qy 353 ADSAKRIKNAVYVNDPNNAIRLRELKBEVTRKDLRAQGLGDI- IDTSMGSLTSS-PSSCSLNS 412
Db 407 LSAISRAAASVSSLERILKFAFGSEARLKESEKRTIAELNETWEEKLRKTEARTEARE 466
Qy 413 -TPLEKQIVSIQPDATVYK-KSKAKAEIVQNLQSEKLYRDUNQWTEELKATEEIIHKE 470
Db 467 ALLAEKGVNAREDDGTIGVFPKPKTHLVNLNEDPLMSECLLYIKDGITRVGQADAEER 526
Qy 471 AALBELGISI-ERK-FYGPVGYHSKEMPHVNLNEDPLMSECLLYIKDGITRVGQADAEER 528
Db 527 QDIVLSGHFKEEHCIFRSDSRGSGEAVVTLPEKSEYTYNGKRVKVPQVLRNSRITNGKXH 586
Qy 529 AELRNGSKILKEHCTF--EN---VDNVTVIPNKAADVWVNGVRIDKPTRLSRGYRIIL 583
Db 587 GKSHVFNHPQARARE 605
Qy 584 GDFHIFRNHPQARAREQ 602

RESULT 3 JN0114 #type complete
ENTRY Kinesin-related protein unc-104 - Caenorhabditis elegans
TITLE #formal_name Caenorhabditis elegans
ORGANISM 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change
DATE 29-May-1998
ACCESSIONS JN0114
REFERENCE Otsuka, A.J.; Jeyaprakash, A.; Garcia-Anoveros, J.; Tang,
#authors L.Z.; Fisk, G.; Hartshorne, T.; Franco, R.; Born, T.
#journal Neuron (1991) 6:113-122
#title The C. elegans unc-104 gene encodes a putative kinesin heavy
chain-like protein.
#cross-references MIM:91097805
#accession JN0114
#molecule_type RNA
#residues 1-1584 #label OTS
#cross-references GB:M58582
#note 598-Thr and 930-Met were also found
GENETICS unc-104
CLASSIFICATION #superfamily kinesin-related protein unc-104; kinesin motor
domain homology; plectatrin repeat homology
KEYWORDS ATP; microtubule binding; P-loop
FEATURE 4-353
93-100
1285-1287
99
SUMMARY
Query Match 36.4%; Score 1975; DB 1; Length 1584;
Best Local Similarity 52.6%; Pred. No. 0.00e+00;
Matches 318; Conservative 123; Mismatches 126; Indels 38; Gaps 20;

Db 2 SSVKAVAVRPFNSRMSRSDSKCIOMSGSTTVNPE-----G--HSTKE-N-F-----SNF 49
Qy 5 GNKKVAVRPFNSRMSRSDSKCIOMSGSTTVNPE-----G--HSTKE-N-F-----SNF 64
Db 50 DHSYNSFARNDPHTITQVQVEELGVEMLEHAFEGYVNCIFAYGTGAGKSYTMCKAND 109

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QY      65 DRSYWSFQKNAFYARQEDLFDGLGVPLLDNAFKNYCINCFAYGQTGSGKSYSMWG--YG 122
      110 PDENGIFPRICNDLFARIDN--NNDKDVQSVSEVSYMEIYCVKVDLLNPNSGGNLRVREH 168
      123 KEH-GVIFRICQDMFRINELQDKNLCTCTVEVSYLETYNERNVRLDLPNFTSGNKLKVRH 181
      169 PLLGYPVDDUTLKMAVCSYHDICNLMDEGNKARTVAATNNMNSTSSRSHAVFTVLTKRHC 228
      182 PSTGYPVEDLAKLVRSQEIENLMDENKARTVAATNNMNSTSSRSHAVFTVLTKRQHD 241
      229 ADSNLDTKHSKLSIVDLASERANSTGABOORLKEGANTKSLTTLGLVLSKLAESTK 288
      242 EETHMDTKERKAKLSIVDLASERASTGATGAKLREGEINSLSTLGRVYALADANSSG 301
      289 KKSNGKGVIPYDSVLTWLLRENIGNSKTMALASPADINFDFTLSTLYADRAKIV 348
      302 KQKKNQ--LVPRYDSVLTWLLKSLGNSMTAMTAISPADINFEETLSTLYADSAKRIK 360
      349 QOAVYNEDPNAKLRELNEEVIKLRHLKDKG-----IDVTD--VOET--PGK--HKK-G 396
      361 NHAVYNEDPNARMLRELKEALQSLKSSGGGGAGGSGGPVEESYPDPDTPLEKQIV 420
      397 P-KLP-ARHV-----EQL-EKLOESKLMAEIGTWOKLIHTEIRKOREELRDMGLAC 449
      421 STQOPDATYKMKSAEIVQSLNOSKLYRDLNQTWEKLAKEETIHKEREAALEELGIS- 479
      450 AEDGTTGLVSPKPLPHLVNEDPLMSGLIYYLKEGVTSVGRPEAEHRPDLISGEAI 509
      480 IETKGF-VGPHSKEMPHLVNDSPLLAELCYVNTPKGTNRGVNQNQTOAEIRLNGSKI 538
      510 LEHCETINEDGVTPLMKPNASCYINCKQVTPYVLHSGSVTLGCEHVFYKNDOPAR 569
      539 LKEHCETENVNVNVIYVNEKAAVWNGVRIDKPTRLSSGYRIILGDPHFIRENHPPEAR 598
      570 QSRHN 574
      599 AERQE 603

RESULT      4
ENTRY      T13822      #type complete
TITLE      kinesin-like protein unc-104 - Caenorhabditis elegans
ORGANISM   T13822      #formal_name Caenorhabditis elegans
DATE       20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
ACCESSIONS T13822
REFERENCE   T13842
AUTHORS     Du Z.
SUBMISSION  submitted to the EMBL Data Library, February 1996
DESCRIPTION The sequence of C. elegans cosmid C52B12.
ACCESSION   T13822
STATUS      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   1-1584 #label DUZ
#cross-references EMBL:U50135; NID:g1208884; PID:g1208885;
                  PTDN:AAA93453.1; CESP:unc-104
GENETICS
#gene       CESP:unc-104
#introns    3471; 84/2; 140/3; 200/2; 285/3; 339/2; 430/2; 580/1; 631/3;
                  672/1; 738/2; 782/2; 856/3; 902/1; 942/2; 991/3; 1045/2;
                  1236/3; 1352/3; 1397/1; 1545/2
SUMMARY     #length 1584 #molecular-weight 179649 #checksum 6627
Query Match      36.4%; Score 1971; DB 2; Length 1584;
Best Local Similarity 52.4%; Pred. No. 0.00e+00;
Matches 318; Conservative 127; Mismatches 127; Indels 38; Gaps 20;

QY      2 SSVKAVVRFPNORETSNCKVLGVNGTNTTN--G--HSINKE-N-F-----SPNF 49
      5 GNIAVVRVRFNAREIDRGAKIVRMEGNTLTPPPGAEKARKSGKTIWDGPKAF 64
      50 DRSYWSFARNDFPHITOKOVYEEELGVENLHAFBGYNVICFAYGQTGSGKSYTMCKAND 109

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QY      65 DRSYWSFQKNAFYARQEDLFDGLGVPLLDNAFKNYCINCFAYGQTGSGKSYSMWG--YG 122
      110 PDENGIFPRICNDLFARIDN--NNDKDVQSVSEVSYMEIYCVKVDLLNPNSGGNLRVREH 168
      123 KEH-GVIFRICQDMFRINELQDKNLCTCTVEVSYLETYNERNVRLDLPNFTSGNKLKVRH 181
      169 PLLGYPVDDUTLKMAVCSYHDICNLMDEGNKARTVAATNNMNSTSSRSHAVFTVLTKRHC 228
      182 PSTGYPVEDLAKLVRSQEIENLMDENKARTVAATNNMNSTSSRSHAVFTVLTKRQHD 241
      229 ADSNLDTKHSKLSIVDLASERANSTGABOORLKEGANTKSLTTLGLVLSKLAESTK 288
      242 EETHMDTKERKAKLSIVDLASERASTGATGAKLREGEINSLSTLGRVYALADANSSG 301
      289 KKSNGKGVIPYDSVLTWLLRENIGNSKTMALASPADINFDFTLSTLYADRAKIV 348
      302 KQKKNQ--LVPRYDSVLTWLLKSLGNSMTAMTAISPADINFEETLSTLYADSAKRIK 360
      349 QOAVYNEDPNAKLRELNEEVIKLRHLKDKG-----IDVTD--VOET--PGK--HKK-G 396
      361 NHAVYNEDPNARMLRELKEALQSLKSSGGGGAGGSGGPVEESYPDPDTPLEKQIV 420
      397 P-KLP-ARHV-----EQL-EKLOESKLMAEIGTWOKLIHTEIRKOREELRDMGLAC 449
      421 STQOPDATYKMKSAEIVQSLNOSKLYRDLNQTWEKLAKEETIHKEREAALEELGIS- 479
      450 AEDGTTGLVSPKPLPHLVNEDPLMSGLIYYLKEGVTSVGRPEAEHRPDLISGEAI 509
      480 IETKGF-VGPHSKEMPHLVNDSPLLAELCYVNTPKGTNRGVNQNQTOAEIRLNGSKI 538
      510 LEHCETINEDGVTPLMKPNASCYINCKQVTPYVLHSGSVTLGCEHVFYKNDOPAR 569
      539 LKEHCETENVNVNVIYVNEKAAVWNGVRIDKPTRLSSGYRIILGDPHFIRENHPPEAR 598
      570 QSRHN 574
      599 AERQE 603

RESULT      5
ENTRY      T13827      #type complete
TITLE      kinesin-73 - fruit fly Drosophila melanogaster
ORGANISM   T13827      #formal_name Drosophila melanogaster
DATE       20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
ACCESSIONS T13827
REFERENCE   T13842
AUTHORS     Li, H. P.; Liu, Z. M.; Nirenberg, M.
SUBMISSION  Proc. Natl. Acad. Sci. U.S.A. (1997) 94:1086-1091
DESCRIPTION Kinesin-73 in the nervous system of Drosophila embryos.
ACCESSION   T13827
STATUS      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-1921 #label LIH
#cross-references EMBL:U81788; NID:g1906595; PID:g1906596;
                  PTDN:AAB50404.1
SUMMARY     #length 1921 #molecular-weight 215047 #checksum 9262
Query Match      29.5%; Score 1597; DB 2; Length 1921;
Best Local Similarity 59.6%; Pred. No. 1.82e-262;
Matches 238; Conservative 66; Mismatches 84; Indels 11; Gaps 8;

QY      1 MASD-KIKYAVVRFPNOREIDETICTIVNEKQOTLONPP-PLEKTER-K--Q-PK 52
      1 MSGCCKIKYVVRFPNAREIDRGAKIVRMEGNTLTPPPGAEKARKSGKTIWDGPK 60
      53 TPAFDHCKLVNLPDENPENSQVFCQVILDNAPQYNACIFAYGQTGSGKSYTMWG 112
      61 AFADBSYNSFDKNAPYARQEDLFDGLGVPLLDNAFKNYCINCFAYGQTGSGKSYSMWG 120
      113 TQESGIIIPRLCDFSIAN-KSTPELMYKVEVSYMEIYKVDLLDPKPNQSLKVR 171

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QY 356 RIKNHAVNEDPNARMRELKEELAQLRSLQSSGGG 397

RESULT 7
ENTRY TITLE S3982 *type complete
ALTERNATE_NAMES kinesin-related protein knp95 - sea urchin
ORGANISM (Strongylocentrotus purpuratus)
#formal_name Strongylocentrotus purpuratus #common_name
DATE 10-Sep-1999 sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S3898 & S72551
REFERENCE S38982, S72551
#authors Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.,
Scholey, J.W.
#journal Nature (1993) 366:268-270
#title Novel heterotrimeric kinesin-related protein purified from
sea urchin eggs.
#cross-references MUID:94050179.
#accession S38982
#molecule_type mRNA
#residues 1-699 #label COL1
#cross-references EMBL:I16993; NID:g295245; PIDN:AAA16098.1;
#accession S72551 PID:g295246

COMPLEX heterotrimer of a 115K chain and two kinesin-related chains
COL2
#molecule_type protein
#residues 2-5,'X',7-11:59-64;125-132;222-226,'X',228-230 #label

CLASSIFICATION
FEATURE
11-348 #domain kinesin motor domain homology #label KMOT\
97-104 #region nucleotide-binding motif A (P-loop)\
103 #binding_site ATP [lys] #status predicted
SUMMARY #length 699 #molecular_weight 78697 #checksum 1222

Query Match 18.6%; Score 1008; DB 1; Length 699;
Best Local Similarity 45.0%; Pred. No. 1,11e-152;
Matches 182; Conservative 86; Mismatches 111; Indels 25; Gaps 15;

Db 6 SGDNVVRVVRCRLNSKETGOGFSVKVMDEMRC -TVOV-TNPAP-SG-----EPPKS 57
QY 2 SGGNLIKVVVRVPNAERDRAICIVRMEGNQTILPPPGAEKKARKSGTMDGPKA 61
Db 58 FTFD-T-VF---AGC-AKQTDVYNQARPVDVAIIISNGTIPAYGTGCTKTWEG- 109
QY 62 FADSNYSWDKNPNARYEDFDLGVLDDNPAFGKNCIFYAGTGSGTSXMMGY 121
Db 110 VRQPQLRGIIPNSAIFGHIAKQENRVFLRVSYLEIYNEEVKOLLCKQQHRLEVK 169
QY 122 GKGVGVPRICQMFR-I-NELQRQ-LNCTCVESYLEINERVOLDLPSTKGNLKVR 179
Db 170 ERPDGVYVVDLSAFVNWADDMDRIPLGNKRVSYGATNMESSSHAIFTIL-EPS 228
QY 180 EHSFTGTPVDLANVRSQLENLDGDKRKARTYANNNTSSSHAFLLITQKW 239
Db 229 DMETLQEQHRYCKLVHVDLAGSRQTKTGCOBLEKFKNLISLTGVISSLYDV-- 286
QY 240 HDEETKMTQEKVAKISLVDLASSERATSTGATGARLEKGEIRNLSLTGLRVIALDMS 299
Db 247 -GR -STH -IPYENSKURLLODSLGGNKATVMCANIGPAYNYDETISTLAYANAKNI 342
QY 300 SGKOKNQLPYRDSVTWLKLKSLGGNSTAMIAAISPADINFEEITSLTSLAYASAKRI 359
Db 343 KNKAKINDFKDALREFQKEIEELKKOISEGGLDDESGS 386
QY 360 KNAVNVNEDPNARMRELKEELAQLRSLQSSGGGAGGGG 403

RESULT 8 B44259 #type complete
 ENTRY kinesin-related protein KIF3A - mouse
 TITLE #formal_name Mus musculus #common_name house mouse
 ORGANISM 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change
 DATE 22-Jun-1999
 ACCESSIONS B44259; S27872
 REFERENCE A44259
 #authors Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
 #journal J. Cell Biol. (1992) 119:1287-1296
 #title kinesin family in murine central nervous system.
 #citations_references PMID:9307766
 #accession B44259 RNA
 #molecule_type 1-701 #label A12
 #residues 701
 #cross-references EMBL: D12645; NID: g220469; PID: BAA02166.1; PID: d1002656; PID: g220470
 #experimental_source brain
 #note
 #description kinesin-related protein KIF3A (NCBI:118911) heterodimer with KIF3B (PIR: A57107); the KIF3A/3B heterodimer associates with kinesin superfamily-associated protein (KAP3) (PIR: J06161) to form a heterotrimer
 #note
 #function KIF3 complex is a motor protein that provides anterograde fast axonal transport of membranous organelles
 #classification #superfamily kinesin-related protein KIF3; kinesin motor domain homology
 #keywords ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; P-loop
 #feature
 1-358 #domain head globular #status predicted #label HGLV
 13-351 #domain kinesin motor domain homology #label KMTV
 100-107 #region nucleotide-binding motif A (P-loop)
 359-599 #domain helical rod #status predicted #label RODV
 600-701 #domain tail globular #status predicted #label TGLV
 106 #binding_site ATP (Lys) #status predicted
 #summary #length 701 #molecular_weight 80167 #checksum 60
 Query Match 17.7%; Score 962; DB 1; Length 701;
 Best Local Similarity 41.4%; Pred. No. 3.24e-144;
 Matches 196; Conservative 104; Mismatches 137; Indels 36; Gaps 28;

Db 14 NKVYVRCPLNRE - K-SWCY-R-QAV-SY-DEMGTI-TVHDTSSN-EPPKTFPD 64
 QY 6 NKIVYVRFNARDIGACIVYRMEGNQTLTPPPGAEKARKSKTMDGPKAF 65
 Db 65 -T--VP--GPE-SKOLDY-NTARPLIDSLVGGYNGTIFAYGOTGCTKFTWEGVAV 116
 QY 66 RSTWFDKAPNARQEDFDLGV-PLIDNAFNKYNCFAYGOTGSGKSYSMGY-G- 122
 Db 117 PGLAGVINSPIHFHIAKAGDTRFL--VRSYLEIYNEEVRDLGDKDQTOLEVKER 174
 QY 123 KE-GVPIRCPDPRFELNQDKNLTCTVEVSYLNIYNERVRLNPFSTKLNKLVREH 181
 Db 175 PDGVGYIDLSAYVYNADDIMRTMLGHKNRSYGATNMNHSRSHAFITIECEK 234
 QY 182 PFTGVEDLAKLVRSFOTENLMDGKNKARTVAATNMNYSRSHAVFTLTQKWH 241
 Db 235 VDGNEHV-RMGLHLHVLADGSRQAKTGQRKATKINLSLTGHNVISALVD--G 290
 QY 242 EETIMTKETKAKVAKISLVDLAGSERATSTGATGARKGKGAETNRSLSLGRVTAALAD 301
 Db 291 K--5TH-VPKNSKTLRELQSLGNSKTMKNCIGADYNDETISTLYRANAKNK 347
 QY 302 KQKKNQVYRDSVLTWLLKSLGNSNTAMTALSPADINFEETLSTLYRADA 361
 Db 348 KARLNEDPKALLRQFOETELKLEKLEE-GEVYSGDISGSEDDP-EGLEGEDEK 405
 QY 362 HAVYNEDPNARIRELKEBLAQRLKSLQSGGGGGAGGSGVPEESYPTDPLENQIVS 421
 Db 406 KRRQAGKVKVSPKNYE-M-QA-KIDEE-RKALETKIDMEERENKARAELE 454

QY 422 LQOPDQVTKKSKAEIVQQLNSEKLYRLNQTHWEKLAKEEIHKEEAAALE 474
 RESULT 9 S58691 #type complete
 ENTRY kinesin-related protein KRP95 - sea urchin
 TITLE (Strongylocentrotus droebachiensis)
 ORGANISM #formal_name Strongylocentrotus droebachiensis
 DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
 ACCESSIONS S58691
 REFERENCE S58691
 #authors Reshid, D.J.; Wadaman, K.P.; Scholey, J.M.
 #journal Mol. Biol. (1995) 252:157-168
 #title Heterodimerization of the two motor subunits of the heterotrimeric kinesin, KRP(85/95).
 #cross-references MUID: 95404510
 #accession S58691
 #status preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 #molecule_type mRNA
 #residues 1-742 #label RAS
 #description heterotrimer of a 115K chain and two kinesin-related chains of 85K (PIR: S38982) and 95K
 #classification #superfamily kinesin-related protein KIF3; kinesin motor domain homology
 #keywords ATP; heterotrimer; microtubule binding; P-loop
 #feature
 5-345 #region nucleotide-binding motif A (P-loop)
 101 #binding_site ATP (Lys) #status predicted
 #summary #length 742 #molecular_weight 84156 #checksum 2976
 Query Match 17.7%; Score 962; DB 1; Length 742;
 Best Local Similarity 44.5%; Pred. No. 3.24e-144;
 Matches 177; Conservative 86; Mismatches 105; Indels 30; Gaps 18;

Db 5 SAETVYVRCRPNMSKEISQGHRRIVENDKRG-LVEVNP--KGP-PGEP--N--KSF 56
 QY 3 GGGNKVYVVRPNFARNIDRGACIVRMEGNQTLTPPPGAEKARKSKTMDGPKAF 62
 Db 57 TFDVYDWN-SKQIDLY---DETRSL-Y--ESVLOGNFTIPAYGOTGCTKFTWEGV 108
 QY 63 AFDRT-WFSDNPNYARQEDFDLGVPLIDNAFNKYNCFAYGOTGSGKSYSMGY 121
 Db 109 RSNPELGIVINSPIHFHIAKAGDTRFL--VRSYLEIYNEEVRDLGDKDQKFDL 165
 QY 122 -GK-B-GVPIRCPDPRFELNQDKNLTCTVEVSYLNIYNERVRLNPFSTKLNK 178
 Db 166 KRPDTGVYVRCPLNRE - K-SWCY-R-QAV-SY-DEMGTI-TVHDTSSN-EPPKTFPD 225
 QY 179 REHPTGVEDLAKLVRSFOTENLMDGKNKARTVAATNMNYSRSHAVFTLTQK 238
 Db 226 ELGVGDENHI-RVGLNIVLADGSRQAKTGQRKATKINLSLGRVTAALVD- 283
 QY 239 WHDETMTKETKAKVAKISLVDLAGSERATSTGATGARKGKGAETNRSLSLGRVTAALAD 298
 Db 284 --CK--SSH-IPYRSKTLRELQSLGNSKTMKNCIGADYNDETISTLYRANAKN 338
 QY 299 SSGKQKNQVYRDSVLTWLLKSLGNSNTAMTALSPADINFEETLSTLYRADA 356
 Db 339 IKMKPKNEDPKALLRQFOETELKLEKLEE-GEVYSGDISGSEDDP-EGLEGEDEK 376
 QY 359 IKHNAVNEPNARIRELKEBLAQRLKSLQSGGGGGAGGSGVPEESYPTDPLENQIVS 396

RESULT 10 A47334 #type fragment
 ENTRY Lckin kinesin-related antigen - Leishmania chagasi (fragment)
 TITLE #formal_name Leishmania chagasi
 ORGANISM 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
 DATE 24-Sep-1999

```

ACCESSIONS A47334
REFERENCE A47334
#authors Burns Jr., J.M.; Shreffler, W.G.; Benson, D.R.; Chailb, H.W.;
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:775-779
#title Molecular characterization of a kinesin-related antigen of
# Leishmania chagasi that detects specific antibody in
# African and American visceral leishmaniasis.
#cross-references MUID:93133867
#accession A47334
#status preliminary
#molecule_type DNA
#residues 1-955 #label BUR
#cross-references GB:L07879; NID:9308884; PIDN:AAA29254.1; PID:g308885
#experimental_source MROW/BR/82/BA-2.C1
#note sequence extracted from NCBI backbone (NCBIN:122864,
# NCBIP:122865)
CLASSIFICATION #superfamily unassigned kinesin-related proteins; kinesin
#motor domain homology
KEYWORDS ATP; P-loop
FEATURE
13-398 #domain kinesin motor domain homology #label KMO7N
122-129 #region nucleotide-binding motif A (P-loop)
#length 955 #checksum 7462
SUMMARY
Query Match 17.6%; Score 953; DB 2; Length 955;
Best Local Similarity 43.5%; Pred. No. 1.46e-142;
Matches 177; Conservative 90; Mismatches 111; Indels 29; Gaps 18;
Db 13 VKVSVVRVRERENNAPEGTQVTVAAKQAAAVVYKVLGGSNNGAAESMGTRARVAQD 72
QY 7 IKVVRVHPFAHEID-R-GAKCIVR-MEGNQT1-LTPPPGAEEKARSGK-TIMDGPKA 61
Db 73 PQDHFVSVETPDACGATPATQADVPRTIGYVPLVQHAFDGFNSCLFAYGOTSGKTYTM 132
QY 62 FADFNSYFSDK-NA-PNY-AQEDLFQDLGVPLLDNAFKYNCIFAYGOTSGKSYSM 118
Db 133 MGADVSALSGEGNVPTRICLEIFARKASVAAQGSNWTVELGVVEYVNRVSDLLGKRK 192
QY 119 MG-----NL--KVRHPTGPGYEDLAKLV-VRSFQELNLDGSKARTVAATNMET 223
Db 193 KGVKGGEYVDVREHPSGVFLG-QLRVESGLDDVRLVLEIGNGVRTASTAMDR 251
QY 171 -STKG---NL--KVRHPTGPGYEDLAKLV-VRSFQELNLDGSKARTVAATNMET 223
Db 252 SSBSHAILMLLEERTWTKSGEITFACKSSRNVLVDLGSERVAQSVQEGQPKAT 311
QY 224 SSBSHAYTLTLTKW-----HDEETKMDTEKVAKLSVLDLGSERATSTGATGARLGEA 279
Db 312 HINLSITTLGRVLDVADMTAKAQYVAFPDGKLFILDKSLGNSFTKATATSP 371
QY 280 EINRSLSITGRVLAADMSG-GKQKNQVLPYRDSVLVLLKSLGNSMTAMIAISP 338
Db 372 SALNVEETLSTLYASARDIVNVAQNDPAPRRIRLELEQMDMR 418
QY 339 ADINEETLSTLYADSARKINHAVDNPAPRRIRLEKELAQLR 385
RESULT 11
ENTRY #type complete
TITLE kinesin-related protein KIF3B - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change
22-Jun-1999
ACCESSIONS A57107
REFERENCE A57107
#authors Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.
#journal J. Cell Biol. (1995) 130:1387-1399
#title KIF3A/B: a heterodimeric kinesin superfamily protein that
# works as a microtubule plus end-directed motor for membrane
# organelle transport.
#cross-references MUID:96032268
#accession A57107
#status nucleic acid sequence not shown
#molecule_type mRNA
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-747 #label YAM
#cross-references GB:D26077; NID:g1060922; PIDN:BA05070.1;
#cross-references PID:g10605611; PID:g1060923
#experimental_source brain
#complex heterodimer with KIF3A (PIR:B44259); the KIF3A/3B heterodimer
# associates with a kinesin superfamily-associated protein
# (KAP3) (PIR:JC6161 in testis) to form a heterotrimer
FUNCTION
#description KIF3 complex is a motor protein that provides anterograde
# fast axonal transport for an unknown cargo
#superfamily kinesin-related protein KIF3; kinesin motor
#domain homology
KEYWORDS ATP; coiled coil; heterodimer; heterotrimer; microtubule
#binding; P-loop
FEATURE
1-363 #domain head globular #status predicted #label HGL\
10-346 #domain kinesin motor domain homology #label KMO7N\
96-103 #region nucleotide-binding motif A (P-loop)\
364-592 #domain helical rod #status predicted #label ROD\
594-747 #domain tail globular #status predicted #label TGL\
102 #binding_site ATP (Lys) #status predicted
SUMMARY #length 747 #molecular-weight 85288 #checksum 7951
Query Match 17.4%; Score 942; DB 1; Length 747;
Best Local Similarity 46.7%; Pred. No. 1.53e-140;
Matches 163; Conservative 73; Mismatches 99; Indels 14; Gaps 9;
Db 37 KLGQSVKPKGSHENPKFTFTFDVYDMNAKQFELXDETERPLVDSVLQGFNGTIFAYG 96
QY 50 KSKGKTMDGPKAFADRS-YWGFDKNAPYARQEDLFQDLGVPLLDNAFKYNCIFAYG 108
Db 97 QTGKTGTYMEGVGRDPEKGVPSFDFHFTTHSRNQOYL---VRSVSLYEYEEIR 153
QY 109 QTSKGSQVSMGY-GK-E-RGVIPRCQDMFRINELQDKNKLCTVFEVSLYEYENVR 165
Db 154 DLLSKDQTKLELRPDTGVYVVDLSFVTKSVKEIEHVMNVGNVGNVSGVATNMHSS 213
QY 166 DLLNPSTKGNLVKRGHSTPGYVEDLAKLVRSFQELNLDGSKARTVAATNMETSS 225
Db 214 RSHAFVPTI-ECSVEVDGENHIVKGLNLVDLAGSERQAKTGQGERLKEATKLNLSL 272
QY 226 RSHAVFTLTITQKHDEETKMDTKQVAKLSVLDLAGSERATSTGATGARLGEAENRSL 285
Db 273 SALGNVISALVD---GK--STH-IPYRDSKLTRLQDSLGNNATVYVNVGNVPASTNVEE 326
QY 286 STLGRIYALADMSGKQKNQVLPYRDSVLVLLKSLGNSMTAMIAISPINFEE 345
Db 327 TLTLTYANPAKINRPNVEDPKDALLREFOEILARKAQLKESIG 375
QY 346 TLSTLYADSARKINHAVDNPAPRRIRLEKELAQLRKLSQSSGG 394
RESULT 12
ENTRY #type fragment
TITLE kinesin-related protein 95k chain - sea urchin
ORGANISM #formal_name Strongylocentrotus purpuratus (fragment)
#common_name purple sea urchin #common_name common_name
DATE 07-Oct-1994 #sequence_revision 07-Feb-1997 #text_change
10-Jul-1998
ACCESSIONS S38983; S72552
REFERENCE S38983
#authors Cole, D.G.; Chinn, S.W.; Wedaman, K.P.; Hall, K.; Vuong, T.;
# Schooley, J.M.
#journal Nature (1993) 366:268-270
#title Novel heterotrimeric kinesin-related protein purified from
# sea urchin eggs.
#cross-references MUID:94050179
#accession S38983
#status nucleic acid sequence not shown
#molecule_type mRNA

```

```

11-359      #domain kinesin motor domain homology #label KNOTV
97-104      #region nucleotide-binding motif A (p-loop)
SUMMARY      #length 766 #molecular-weight 86671 #checksum 3764

Query Match      16.0%; Score 870; DB 2; Length 786;
Best Local Similarity 40.0%; Pred. No. 2,37e-127;
Matches 187; Conservative 105; Mismatches 138; Indels 38; Gaps 22;

  Db      6 GGSESVKVVYRCPPLNGEKADGRSRIVDMO---V-DA--G-QVKVKNPKADASEPPKA 57
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      2 SGGGNKIKVYVRFPNFAREIDRGAKCIKRMGEQNTILTPPPGAEKARKSKTINDGPKA 61
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      58 TTFDQVY---DNNCOQ--R--DVEDITAPRLDISCIENGYNTIFAYGTGQKGSIMES- 109
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      62 FAPFDSYNSDKAPNPAQEDLQDGLVPLDNNFAGNCFATGYTGSGKASIMGT 121
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      110 KDFPELRLGTLTFYVFLTARSDTGEFLVRESYLEYVETNEVYVOLLKQHSKMKELK 169
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      122 KGEHGVPRICQDMERINEL-QDKNLT-CTVENSYLEYINERVRLNLSLTKGLKVR 179
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      170 ESPDGVVYVADLSQFVCKNVEENKVKLLAGDKADNRQVATLMMQDSRSRHSIFITIECE 229
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      180 EHPSTGPGVDELAKLVRSFQETENLMDGKNARTVAATNMNNTSSRSNAVFVTL--TQ 237
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      230 KLESAAGKPGAKDDSHNVYRGKLNLDLAGSERDQKTGATGORKLGNKLNLSLTALG 289
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      238 KWHDE--E--TKMD-TE-KVAKISLDVLAGSERATSTGATGARLKEGAEINRSLSLTG 289
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      290 WYISALVD--CK--SGH-IPYDSKTLRLQDSLGQWYVYVANIQPADWDETMTST 343
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      290 RYVALADMSQKKNQVYVDSVYVLLADLSGNSHTAMTALSPADINFEETLST 349
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      344 LRYANRANTONKPKEDKDALRFOFEIKLKEQLAARAGGSGPI-TM-PSGGS 401
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      350 LRYADSARKKHAVVNEPDMRIKELAEQLARSLQSSGGGGGAGGGGSGPVEEY 409
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      402 PTKQIVER--TEEVDPDIDAKIQAOMRLAEKMK-SDISTEALDKAREE 447
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Db      410 PPDTPLEKQIVSIQDPATVTKKSKASIVEQLNOSEKLYRLDNLQTMEE 457
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      15
ENTRY      T13750      #type complete
TITLE      kinesin-like protein 38B - fruit fly (Drosophila
ORGANISM   melanogaster)
ACCESSIONS #forma_1gene Drosophila melanogaster
REFERENCE   13-Aug-1999      #sequence_revision 13-Aug-1999 #text_change
#authors    T13750
#journal    Ohkura, H.; Torok, T.; Tick, G.; Hoheisel, J.; Kless, I.;
#title      Glover, D.M.
#accession  J. Cell Sci. (1997) 110:945-954
#status     Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#realdues  1-1121 #label OHK
#cross-references EMBL:Y10667; NID:e1054562; PTD:e1192009;
#PDB:CAK71675.1

GENETICS
#2-position 2
SUMMARY      #length 1121 #molecular-weight 125194 #checksum 7078
Query Match      15.8%; Score 857; DB 2; Length 1121;
Best Local Similarity 37.3%; Pred. No. 5,60e-125;
Matches 243; Conservative 147; Mismatches 179; Indels 83; Gaps 42;

  Db      115 VSESHNIVAVRPRLNALECTGQVNVVGVGNSNELVQAGSADAS-AG--VTH-- 169
  Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  Qy      1 MSGGGNKIKVYVRFPNFAREIDRG-AKCIVRMEGNTILTPPPGAEKARKSKTINDGP 59

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Db      170 -TFSDQVYVSCDPERKNFAQAFVECTARDPLDPAFESYNACLFAYGQSGSKSYSM 228
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      60 KAPAFDSYNSDKAPNPAQEDLQDGLVPLDNNFAGNCFATGYTGSGKASIMGT 119
Db      229 GTEALDAAALDGGPPHDEAGIIPRPFCELEPRRIEAVKSOQLOVEVEVSYFEIYNKTHD 288
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      120 GY-G-K---E---H---GVPIRQCQDMERINELQDKNLTCTVEVSYLEYINERVRLD 166
Db      289 LLSVQHAHAATGESPTIQOQOQOQORPALKVREHPFGVYVLDLSAHSVDSYSALRNMLAV 348
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      187 LL--NPST-KGN-----LKVREHFPSTGPGVDELAKLVRSFQETENLMD 208
Db      349 GNSORATATAMKDSRSRHSIFNIVLNTLDLSDDGLSSDTSSTASSLRTRRSKLSL 408
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      209 GNAKRTVAATNMNNTSSRSNAVF--LTQL-KWHD---E-ETKMQTE-K-V--AKISL 256
Db      409 VOLAGSERISVCSNGSRITRECVSYTNKSLTGLKVTAAALADSKASANGPLSGTSTFV 468
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      257 VOLAGSERATSTGATGARLKEGAEINRSLSLTGLRVTAALD--MSSGK-Q--K-K-NQLV 309
Db      469 PYRESVLTMLRENILGNSKTVMLATISPASIHAEDELATLRYACKARSI VNRVKNVNSP 528
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      310 PYRDSVLTMLKDSLGNSKMTAATISPADINFEETLSTLRYADSARKKHAVVNEDP 369
Db      529 HDKIIRLRAEVDRLKS-LRNEYERORRL--SGNS-NNPVPRKIIET---SYDETE--V 579
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      370 NARMIRLEKEELAQRLSKLQSSGGGGGAGGGGPGVEESYPDTPLEKQIVSIQDPATV 429
Db      580 EAL-ROQLAER--ERE-LSRA-QKSMKELKKAEDQKSELRYLKRGLALE--LTAE-Q 631
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      430 KNSKAEIPEQLAQSEALRDNLNPTWEKLANTEILIKREALBELUGISTEKFGVGPYH 489
Db      632 -KQ-ACLYNLTADPTLSLTGLVLLPQGLVRCGRGLPGCSSSOPDVLGDLPLVALQHS 689
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      490 SKEMPHVNLSDPDLAELCLVYNIKPGQTRVG-N-V---NODTQAEIRLNGSKILKEHCT 544
Db      690 IEHBERGKLYVDPGSEDFETVYVNGELLAKDRRLPHGDRVLVGGSHYFRISNP 741
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      545 FENV-DNVVTIVP-NEKAAVYVNGVRIDKPTRLRSRGYRILIGDPHIFRPNHP 594

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Search completed: Mon Aug 21 15:40:03 2000
Job time : 44 secs.

```

##residues      1-294 ##label COL1
##cross-references GB:U00996
#accession      S7252
#molecule_type protein
##residues      247-264 ##label COL2
CLASSIFICATION  #superfamily kinesin-related protein KIF3; kinesin motor
domain homology
P-loop
KEYWORDS
1-279           #domain kinesin motor domain homology (fragment) #label
SUMMARY
29-36           #region nucleotide-binding motif A (P-loop)
#length 294 #checksum 4908
Query Match      16.6%; Score 900; DB 2; Length 294;
Best Local Similarity 48.7%; Pred. No. 7.69e-133;
Matches 148; Conservative 66; Mismatches 77; Indels 13; Gaps 8;

Db 1 KOIDYDFTRSLVESVLOGFNGTIFAYGQTGKTFTMEGVSRNPELRGVIPNSFEHIF 60
QY 80 RQEDFDQGVLPDNNAFNGNINCFAYGQTGSGKSYSMGY-GK-E-HGVIPRICQDMF 136

Db 61 THIAITQSOQFL---VRASYLEIYQEEIRDLDAKKDLKRPDGVGVVXDLSSFTV 117
QY 137 RRIEIAQKDKNTCTVEVSYLEIYNERNVDLLNPFSTKGNLKVREHPSTGYPVEDLAKLV 196

Db 118 KSWKEIEHVMTYGNNSVSGSTNNNHSRSHAFITITIECSLGVGDENHI-RVYKLN 176
QY 197 RFQFIENLMDGKAKRTVAATNNNETSSRSHAVFTLTQKWHDET-KMDTEKVAKISL 256

Db 177 VLAGSERQAKTGATGDRKLEATKINLSLSALGNVTSALVD---GK--SSH-IPYRQSKL 230
QY 257 VLAGSERATSTGATGARLKEGAEINRSLSLTGLVTAALADMSGKQKQLNPYRDSVL 316

Db 231 TRLQDSLGGNAKTVVWVNGKPSYFNFDITITLYANRANKNKNKINEDPKALLRE 290
QY 317 TWLKDLSGNSMTAIAISPADINFEETLSTLYRADSARIKKNHIAVVEDNARMIRE 376

Db 291 FOEE 294
QY 377 LKEE 380

RESULT 13
ENTRY          A5236 #type complete
TITLE          kinesin-related protein KLP68D - fruit fly (Drosophila
ALTERNATE_NAMES melanogaster)
ORGANISM       #formal_name Drosophila melanogaster
DATE           23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
ACCESSIONS     A5236; E41298
REFERENCE       A5236
#authors       Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
#journal       J. Cell Biol. (1994) 127:1041-1048
#title         Characterization of the KLP68D kinesin-like protein in
#cross-references MUID:95050960
#accession     A5236
#molecule_type mRNA
##residues     1-784 ##label PES
##cross-references GB:U15974; NID:9595912; PIDN:AAA69929.1; PID:g565090
REFERENCE       A41298
#authors       Stewart, R.J.; Pesavento, P.A.; Moerpel, D.N.; Goldstein,
#journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8470-8474
#title         Identification and partial characterization of six members of
#cross-references MUID:92020874 the kinesin superfamily in Drosophila.
#accession     E41298
#molecule_type DNA
##residues     'TC',222-337,'RGQV' #label STE
##cross-references GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792

```

```

GENETICS
#gene           FlyBase:Klp68D; Klp5
#cross-references FlyBase:FBgn0004381
FUNCTION
#description    may be part of a motor protein that provides anterograde fast
axonal transport
CLASSIFICATION  #superfamily kinesin-related protein KIF3; kinesin motor
domain homology
KEYWORDS
FEATURE
1-349          #domain head globular #status predicted #label HGL\
20-350         #domain kinesin motor domain homology #label KMOT\
106-113        #region nucleotide-binding motif A (P-loop)\
350-580        #domain helical rod #status predicted #label ROD\
581-784        #domain tail globular #status predicted #label TGL\
112            #binding site ATP (Lys) #status predicted
SUMMARY        #length 784 #molecular-weight 88193 #checksum 3313

Query Match      16.5%; Score 897; DB 1; Length 784;
Best Local Similarity 46.5%; Pred. No. 2.73e-132;
Matches 152; Conservative 83; Mismatches 72; Indels 20; Gaps 14;

Db 63 QKRVFTDAAYDASATQTLHYHEVVPVLYSLVGGPNCIFAYGQTGKTFTMEGVSRN 122
QY 65 DRSYWFQDNAPVARQEDLFQDLGVPLDNNAFNGYNCFAYGQTGSGKSYSMGY-GK 123

Db 123 DELMGIIIPREFQIWLHIN--RTS-NPQFLVDVSYLEYIMEELRDLKPNKSHLEVRE 178
QY 124 EH--GVIPRICQDMFRINELQKOKNLTCTVEVSYLEIYNERNVDLLNPFSTKGNLKV 181

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QY 182 PSTGYPVEDLAKLVVRSFQFIENLMDGKAKRTVAATNNNETSSRSHAVFTLTQKWH 241

Db 236 TET--NTIKVGLKLNILDLAGSRQSTKGASAEKLEKASKINLSLGNVTSALAE-SS- 291
QY 242 EETKMDTEKVAKISLVDLAGSRATSTGATGARLKEGAEINRSLSLTGLVTAALADMSG 301

Db 292 P---H-VPYRDSKLTRLQDSLGGNSKTIIMANIGPSNYNYNETITLYRGSRAKSN 346
QY 302 KQKKNQLVPYRDSVLTLTKDLSGNSMTAIAISPADINFEETLSTLYRADSARIKKN 361

Db 347 QPIKNEPQDAKLEKEYOEIERLK-RL 372
QY 362 HAVVNEPDPNARMIRELKEELAQLRSKL 388

RESULT 14
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ORGANISM       #formal_name Chlamydomonas reinhardtii
DATE           07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
ACCESSIONS     A53939
REFERENCE       A53939
#authors       Walther, Z.; Vashishtha, M.; Hall, J.L.
#journal       J. Cell Biol. (1994) 126:175-188
#title         The Chlamydomonas FLA10 gene encodes a novel
#cross-references MUID:94299638 kinesin-homologous protein.
#accession     A53939
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##cross-references EMBL:L33697; NID:g497696; PIDN:AAA21738.1;
PID:g497697
#note          authors translated the codon AAC for residue 753 as Asp
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#gene           FLA10
CLASSIFICATION  #superfamily unassigned kinesin-related proteins: kinesin
motor domain homology
KEYWORDS
FEATURE        ATP; coiled coil; heptad repeat; P-loop

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